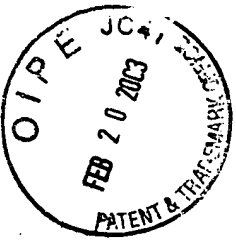


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G-091US05DIV

SEQUENCE LISTING

<110> Benjanin, Stephane  
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

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<140> US 09/992,095  
<141> 2001-11-13

<150> US 09/924,340  
<151> 2001-08-06

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<150> US 60/305,456  
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cggttgccaca gttttgatga tcatctctct cccaaccaag atggtggaaa aagcaaaaac   180
gtggtgaatc ttggagcaat ccgacaaggc atgaaacgct tccaatttct gttaaactgc   240
tgtgagccag ggacaattcc tgatgcctcc atcctagcag ctgccttggg tctactatgc   300
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tcgttaaaaag gtactgtgaa cccctctaaa tgcggttgcc cctttgcctt gaag atg   1437
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gca gca tgt cag ctt ctt ctg gag att acc acc ttc ctg cga gag acc   1485
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ttt tct tgc ctg ccc aga cct cgc act gag cct ctg gtg gct tca acg   1533
Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser Thr
      20                      25                      30

gac cac acc aaa atg cca tct caa atg gaa cac gcc atg gaa acc atg   1581
Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met
      35                      40                      45

atg ttt aca ttt cac aaa ttc gct ggg gat aaa ggc tac tta aca aag   1629
Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr Lys
      50                      55                      60                      65

gag gac ctg aga gta ctc atg gaa aag gag ttc cct gga ttt ttg gaa   1677
Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu Glu
      70                      75                      80

aat caa aaa gac cct ctg gct gtg gac aaa ata atg aag gac ctg gac   1725
Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp
      85                      90                      95

cag tgt aga gat ggc aaa gtg ggc ttc cag agc ttc ttt tcc cta att   1773
Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu Ile
      100                      105                      110

gcg ggc ctc acc att gca tgc aat gac tat ttt gta gta cac atg aag   1821
Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys
      115                      120                      125

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cag aag gga aag aag taggcagaaa tgagcagttc gctcctccct gataagagtt 1876  
 Gln Lys Gly Lys Lys

130

gtcccaaagg gtcgcttaag gaatctgccc cacagcttcc cccatagaag gatttcatga 1936

gcagatcagg acacttagca aatgtaaaaa taaaatctaa ctctcatttg acaagcagag 1996

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20 25 30

Thr Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr

35 40 45

Met Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr

50 55 60

Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu

65 70 75 80

Glu Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu

85 90 95

Asp Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu

100 105 110

Ile Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met

115 120 125

Lys Gln Lys Gly Lys Lys

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                                   Met Glu Leu Ala Leu Arg
                                   -25                               -20

cgc tct ccc gtc ccg cgg tgg ttg ctg ctg ctg ccg ctg ctg ctg ggc      104
Arg Ser Pro Val Pro Arg Trp Leu Leu Leu Leu Pro Leu Leu Leu Gly
                                   -15                               -10                               -5

ctg aac gca gga gct gtc att gac tgg ccc aca gag gag ggc aag gaa      152
Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu
                                   1                               5                               10

gta tgg gat tat gtg acg gtc cgc aag gat gcc tac atg ttc tgg tgg      200
Val Trp Asp Tyr Val Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp
                                   15                               20                               25

ctc tat tat gcc acc aac tcc tgc aag aac ttc tca gaa ctg ccc ctg      248
Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu
                                   30                               35                               40                               45

gtc atg tgg ctt cag ggc ggt cca ggc ggt tct agc act gga ttt gga      296
Val Met Trp Leu Gln Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly
                                   50                               55                               60

aac ttt gag gaa att ggg ccc ctt gac agt gat ctc aaa cca cgg aaa      344
Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys
                                   65                               70                               75

acc acc tgg ctc cag gct gcc agt ctc cta ttt gtg gat aat ccc gtg      392
Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val
                                   80                               85                               90

ggc act ggg ttc agt tat gtg aat ggt agt ggt gcc tat gcc aag gac      440
Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp
                                   95                               100                               105

ctg gct atg gtg gct tca gac atg atg gtt ctc ctg aag acc ttc ttc      488
Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
                                   110                               115                               120                               125

agt tgc cac aaa gaa ttc cag aca gtt cca ttc tac att ttc tca gag      536
Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu
                                   130                               135                               140

tcc tat gga gga aaa atg gca gct ggc att ggt cta gag ctt tat aag      584
Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys
                                   145                               150                               155

gcc att cag cga ggg acc atc aag tgc aac ttt gcg ggg gtt gcc ttg      632
Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly Val Ala Leu
                                   160                               165                               170

ggg gat tcc tgg atc tcc cct gtt gat tgc gtg ctc tcc tgg gga cct      680
Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro
                                   175                               180                               185

tac ctg tac agc atg tct ctt ctc gaa gac aaa ggt ctg gca gag gtg      728
Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys Gly Leu Ala Glu Val
                                   190                               195                               200                               205

tct aag gtt gca gag caa gta ctg aat gcc gta aat aag ggg ctc tac      776
Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr
                                   210                               215                               220

aga gag gcc aca gag ctg tgg ggg aaa gca gaa atg atc att gaa cag      824
Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala Glu Met Ile Ile Glu Gln
                                   225                               230                               235

gta aaa agg gga aac act cag agg cta gcc tgc ttg gct ttt tct ggt      872

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Val Lys Arg Gly Asn Thr Gln Arg Leu Ala Cys Leu Ala Phe Ser Gly
      240                245                250
ggg tac agg gcc cat ggt tgg tgt tgt caa act tgg agt cta cac      917
Gly Tyr Arg Ala His Gly Trp Cys Cys Gln Thr Trp Ser Leu His
      255                260                265
tgaggctccc cacatatctg caaatgattg catgctggat aataaatctc ttgggtctaa 977
gcagtgatgt agtggctcct tacagagtca gaaagccacc caggcctgca agacttgctt 1037
gtccttcact aaatgtatgg attctattaa aaaaaaaaaa aaaa      1081

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Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp Trp Pro
      -10                -5                1                5
Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
      10                15                20
Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn
      25                30                35
Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln Gly Gly Pro Gly Gly
      40                45                50
Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser
      55                60                65                70
Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu
      75                80                85
Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser
      90                95                100
Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met Met Val
      105                110                115
Leu Leu Lys Thr Phe Phe Ser Cys His Lys Glu Phe Gln Thr Val Pro
      120                125                130
Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile
      135                140                145                150
Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn
      155                160                165
Phe Ala Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser
      170                175                180
Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp
      185                190                195
Lys Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
      200                205                210
Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys Ala
      215                220                225                230
Glu Met Ile Ile Glu Gln Val Lys Arg Gly Asn Thr Gln Arg Leu Ala
      235                240                245
Cys Leu Ala Phe Ser Gly Gly Tyr Arg Ala His Gly Trp Cys Cys Gln
      250                255                260

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Thr Trp Ser Leu His  
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tgagtaaaag gactcagcca act atg aag ttt ttt gtc ttt gct tta gtc ttg 113  
Met Lys Phe Phe Val Phe Ala Leu Val Leu  
-15 -10  
gct ctc atg att tcc atg att agc gct gat tca cat gaa aag aga cat 161  
Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His  
-5 1 5  
cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209  
His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile  
10 15 20  
aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257  
Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu  
25 30 35 40  
aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305  
Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe  
45 50 55  
tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357  
Ser Ile Val Thr  
60  
gtactgtttc tgaataatag aaatcacttc tctaaaagca ataaatttca agcacatttt 417  
taaataaaaa aaaaaaaaaa a 438

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 Ile Ser Ala Asp Ser His Glu Lys Arg His His Gly Tyr Arg Arg Lys  
                           1                          5                          10  
 Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe  
          15                          20                          25  
 Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu  
 30                          35                          40                          45  
 Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe Ser Ile Val Thr  
                           50                          55

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   Met Arg Leu Pro Ala Gln Leu  
   -15  
 ctg ggg ctg cta atg ctc tgg gtc tct gga tcc agt ggg gat att gtg 100  
 Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val  
                           -10                          -5                          1  
 atg act cag tct cca ctc ttc ctg ccc gtc acc cct gga gag ccg gcc 148  
 Met Thr Gln Ser Pro Leu Phe Leu Pro Val Thr Pro Gly Glu Pro Ala  
 5                          10                          15                          20  
 tcc atc tcc tgc agg tct agt cag agc ctc ctg cat gtt caa ggg tcc 196  
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Val Gln Gly Ser  
                           25                          30                          35

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aac tat ttg gat tgg tac cac cag aag cca ggg cag tct cca caa ctc 244
Asn Tyr Leu Asp Trp Tyr His Gln Lys Pro Gly Gln Ser Pro Gln Leu
      40                      45                      50
ctg ata tac ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc 292
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
      55                      60                      65
agt ggc agt gga tca ggc aca gat ttc aca ctg aaa atc agt aga gtg 340
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
      70                      75                      80
gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct cta caa act 388
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
      85                      90                      95                      100
cca ttc act ttc ggc cct ggg acc aga gtg gat atc aag cga act gtg 436
Pro Phe Thr Phe Gly Pro Gly Thr Arg Val Asp Ile Lys Arg Thr Val
      105                      110                      115
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 484
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
      120                      125                      130
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 532
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
      135                      140                      145
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 580
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
      150                      155                      160
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 628
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
      165                      170                      175                      180
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 676
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
      185                      190                      195
gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 724
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
      200                      205                      210
aag agc ttc aac agg gga gag tgt tagagggaga agtgccccc cctgctcctc 778
Lys Ser Phe Asn Arg Gly Glu Cys
      215                      220
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cccctattgc ggtcctccag ctcatactttc acctaccccc cctcctcctc cttggcttta 898
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      1                      5                      10

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Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
      15                20                25
Leu Leu His Val Gln Gly Ser Asn Tyr Leu Asp Trp Tyr His Gln Lys
      30                35                40
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala
      45                50                55                60
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
                        65                70                75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
                        80                85                90
Cys Met Gln Ala Leu Gln Thr Pro Phe Thr Phe Gly Pro Gly Thr Arg
      95                100                105
Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
      110                115                120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
      125                130                135                140
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                        145                150                155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
      160                165                170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
      175                180                185
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
      190                195                200
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
      205                210                215

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gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
gccctcaggc ctcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
          Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
                        -10                -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
      1                5                10                15

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atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
                20                25                30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
                35                40                45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
                50                55                60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
                65                70                75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
80                85                90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634
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aagtgtcttt tccaaggcca agctcctgag ggcagg 730

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                5                10                15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
                20                25                30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
35                40                45                50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
                55                60                65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
                70                75                80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
85                90

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<210> 11  
 <211> 733  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..253

<220>  
 <221> CDS

<222> 254..574

<220>

<221> 3'UTR

<222> 575..733

<400> 11

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agatgagtgt tcagctctca gcagagaggt tagctcctct ctgcagcttg tcctgttgtc 60
tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgt 120
gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttcacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
          Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
                    -10                    -5
aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
      1              5              10              15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
                20              25              30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35              40              45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50              55              60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65              70              75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80              85              90
tgagccctga gctaattaag tyctggataa gcatcacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt tattatccac attttgacaga tgaggaaaca gagtcagggtg 694
aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

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<210> 12

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..14

<400> 12

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Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
          -10          -5          1
Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
      5              10              15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20              25              30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35              40              45              50
Tyr His Cys Lys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp

```

```

          55          60          65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
          70          75          80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
          85          90

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<210> 13  
 <211> 732  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> 1..253

<220>  
 <221> CDS  
 <222> 254..574

<220>  
 <221> 3'UTR  
 <222> 575..732

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<400> 13
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tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgct 120
gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
gccctcaggc ctcaggcctt ccctggcttg aagattgggc ttacacctggg acctaccctt 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
          Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
          -10          -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
          1          5          10          15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
          20          25          30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
          35          40          45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
          50          55          60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
          65          70          75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
          80          85          90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634
ctttgaaatg taggtagctt attatccaca ttttgcagat gaggaacag agtcagggtga 694
agtgtctttt ccaaggccaa gctcctgagg gcaggggc 732

```

<210> 14  
 <211> 107

<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..14

<400> 14  
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser  
                           -10                          -5                          1  
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile  
           5  10                          15  
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser  
           20  25                          30  
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg  
 35  40                          45                          50  
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp  
                           55                          60                          65  
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser  
                           70                          75                          80  
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser  
           85  90

<210> 15  
 <211> 733  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..253

<220>  
 <221> CDS  
 <222> 254..574

<220>  
 <221> 3'UTR  
 <222> 575..733

<400> 15  
 agatgagtgt tcagctctca gcagagaggt tagctcctct ctgcagcttg tcctgttgtc 60  
 tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgct 120  
 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180  
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240  
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289  
                           Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala  
   -10  -5  
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337  
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly  
           1  5  10  15  
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385  
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys  
                           20  25  30  
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433

```

Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35              40              45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50              55              60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65              70              75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80              85              90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634
ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcaggtg 694
aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

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<210> 16
<211> 107
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..14

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<400> 16
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
      -10              -5              1
Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
      5              10              15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20              25              30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35              40              45              50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
      55              60              65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
      70              75              80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      85              90

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<210> 17
<211> 1175
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..326

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<220>
<221> CDS
<222> 327..1013

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<220>
<221> 3'UTR

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<222> 1014..1175

<220>

<221> polyA\_signal

<222> 1131..1136

<220>

<221> polyA\_site

<222> 1160..1175

<400> 17

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tgtcagctag acagcagcga ctagggtctcg ggcgcgggccc agatgccttt gttcaccgcc   120
aacccttcgc agcaagacgt ggtgatgcca attggtggaa aggagaaaat cacagaggaa   180
taggactttt cccatccaat ttgttaacaa ctaattttaa catagagact gaggcagcgg   240
ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg   300
agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag   353
                               Met Asp Arg Ala Leu Gln Val Leu Gln
                               1           5
agt ata gat cca aca gat tca aaa cca gac tcc caa gac ctt ttg gat   401
Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp
10                               15           20           25
tta gaa gat atc tgc caa cag atg ggt cca atg ata gat gaa aaa ctt   449
Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu
                               30           35           40
gaa gaa att gat agg aag cat tca gaa ttg tct gaa ttg aat gtt aaa   497
Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys
                               45           50           55
gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca   545
Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro
                               60           65           70
gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct   593
Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro
                               75           80           85
gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt   641
Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly
90                               95           100           105
gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc   689
Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser
                               110           115           120
tat agc cta gga ccc gat caa att ggt cca ctg aga tct ctg cct cca   737
Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro
                               125           130           135
aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta   785
Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu
                               140           145           150
agc act gga caa gac act gtt tcc aat cct act tat atg aac cag aac   833
Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn
                               155           160           165
tct aac cta cag tca gct act ggt aca act gct tac aca cag caa atg   881
Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met
170                               175           180           185
ggg atg tct gtg gat atg tca tct tat cag aac act act tcc aat ttg   929
Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu
                               190           195           200

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cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca      977
Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
      205              210              215
cag cag cac aca aat tac cat cag cag cct ctc ctt tagaaacaaa      1023
Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
      220              225
tcaagcatttt tcttgaaagc cttcataagt gtattattca gtccttgtga taccaacctg 1083
aaaatatataa aacttttttct cctctcaact caaaaggacc atgaataaat aaagcacaaaa 1143
aacctctctt attctgaaaa aaaaaaaaaa at                                1175

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<210> 18
<211> 229
<212> PRT
<213> Homo sapiens

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<400> 18
Met Asp Arg Ala Leu Gln Val Leu Gln Ser Ile Asp Pro Thr Asp Ser
1              5              10              15
Lys Pro Asp Ser Gln Asp Leu Leu Asp Leu Glu Asp Ile Cys Gln Gln
      20              25              30
Met Gly Pro Met Ile Asp Glu Lys Leu Glu Glu Ile Asp Arg Lys His
      35              40              45
Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
      50              55              60
Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
65              70              75              80
Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
      85              90              95
Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser
      100             105             110
Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
      115             120             125
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
      130             135             140
Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
145             150             155             160
Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
      165             170             175
Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
      180             185             190
Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
      195             200             205
Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
      210             215             220
Gln Gln Pro Leu Leu
225

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<210> 19
<211> 844
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..111

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<220>  
 <221> CDS  
 <222> 112..813

<220>  
 <221> 3'UTR  
 <222> 814..844

<400> 19  
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 agcgcgctct gcctgccgcc tgcctgcctg ccactgaggg ttcccagcac c atg agg 117  
 Met Arg  
 -15  
 gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc 165  
 Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala  
 -10 -5 1  
 cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213  
 Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr  
 5 10 15  
 gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg 261  
 Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val  
 20 25 30  
 gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg 309  
 Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val  
 35 40 45 50  
 gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg 357  
 Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val  
 55 60 65  
 tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc 405  
 Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro  
 70 75 80  
 acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat 453  
 Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn  
 85 90 95  
 gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc 501  
 Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys  
 100 105 110  
 acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc 549  
 Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile  
 115 120 125 130  
 ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa 597  
 Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu  
 135 140 145  
 ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg 645  
 Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu  
 150 155 160  
 tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg 693  
 Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu  
 165 170 175  
 cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac 741  
 Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp  
 180 185 190  
 cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg 789  
 His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg

195                      200                      205                      210  
aag gcc aaa atc aag agt gag atg tagaaagttg taaaatagaa aaagtggagt 843  
Lys Ala Lys Ile Lys Ser Glu Met

215  
t 844

<210> 20  
<211> 234  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> 1..17

<400> 20  
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu  
          -15                      -10                      -5  
Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu  
      1                      5                      10                      15  
Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val  
                  20                      25                      30  
Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu  
          35                      40                      45  
Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly  
          50                      55                      60  
Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln  
          65                      70                      75  
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys  
80                      85                      90                      95  
Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr  
                  100                      105                      110  
Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp  
          115                      120                      125  
Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu  
          130                      135                      140  
Thr Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val  
          145                      150                      155  
Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln  
160                      165                      170                      175  
Lys Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala  
                  180                      185                      190  
Gly Asp His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser  
          195                      200                      205  
Ala Arg Lys Ala Lys Ile Lys Ser Glu Met  
          210                      215

<210> 21  
<211> 1997  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> 1..126

<220>  
 <221> CDS  
 <222> 127..1020

<220>  
 <221> 3'UTR  
 <222> 1021..1997

<400> 21  
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 gagttttgtc ccacagtcag caggccacta gtttattaac ttccagtcac cttgattttt 120  
 gctaaa atg aag act ctg cag tct aca ctt ctc ctg tta ctg ctt gtg 168  
 Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Leu Val  
 -15 -10 -5  
 cct ctg ata aag cca gca cca cca acc cag cag gac tca cgc att atc 216  
 Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile  
 1 5 10  
 tat gat tat gga aca gat aat ttt gaa gaa tcc ata ttt agc caa gat 264  
 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp  
 15 20 25  
 tat gag gat aaa tac ctg gat gga aaa aat att aag gaa aaa gaa act 312  
 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr  
 30 35 40  
 gtg ata ata ccc aat gag aaa agt ctt caa tta caa aaa gat gag gca 360  
 Val Ile Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala  
 45 50 55 60  
 ata aca cca tta cct ccc aag aaa gaa aat gat gaa atg ccc acg tgt 408  
 Ile Thr Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys  
 65 70 75  
 ctg ctg tgt gtt tgt tta agt ggc tct gta tac tgt gaa gaa gtt gac 456  
 Leu Leu Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp  
 80 85 90  
 att gat gct gta cca ccc tta cca aag gaa tca gcc tat ctt tac gca 504  
 Ile Asp Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala  
 95 100 105  
 cga ttc aac aaa att aaa aag ctg act gcc aaa gat ttt gca gac ata 552  
 Arg Phe Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile  
 110 115 120  
 cct aac tta aga aga ctc gat ttt aca gga aat ttg ata gaa gat ata 600  
 Pro Asn Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile  
 125 130 135 140  
 gaa gat ggt act ttt tca aaa ctt tct ctg tta gaa gaa ctt tca ctt 648  
 Glu Asp Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu  
 145 150 155  
 gct gaa aat caa cta cta aaa ctt cca gtt ctt cct ccc aag ctc act 696  
 Ala Glu Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr  
 160 165 170  
 tta ttt aat gca aaa tac aac aaa atc aag agt agg gga atc aaa gca 744  
 Leu Phe Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala  
 175 180 185  
 aat gca ttc aaa aaa ctg aat aac ctc acc ttc ctc tac ttg gac cat 792  
 Asn Ala Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His  
 190 195 200  
 aat gcc ctg gaa tcc gtg cct ctt aat tta cca gaa agt cta cgt gta 840

```

Asn Ala Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val
205          210          215          220
att cat ctt cag ttc aac aac ata gct tca att aca gat gac aca ttc      888
Ile His Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe
          225          230          235
tgc aag gct aat gac acc agt tac atc cgg gac cgc att gaa gag ata      936
Cys Lys Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile
          240          245          250
cgc ctg gag ggc aat cca atc gtc ctg gga aag cat cca aac agt ttt      984
Arg Leu Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe
          255          260          265
att tgc tta aaa aga tta ccg ata ggg tca tac ttt taacctctat      1030
Ile Cys Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe
          270          275          280
tggtacaaca tataaatgaa agtacaccta cactaatagt ctgtctcaac aatgagtaaa 1090
ggaacttaag tattgggttta atattaacct tgtatctcat tttgaaggaa tttaatattt 1150
taagcaagga tggtcaaaat cttacatata ataagtaaaa agtaagactg aatgtctacg 1210
ttcgaaacaa agtaatatga aaatatttaa acagcattac aaaatcctag tttatactag 1270
actaccattt aaaaatcatg tttttatata aatgcccaaa tttgagatgc attattccta 1330
ttactaatga tgtaagtacg aggataaaatc caagaaactt tcaactcttt gcctttcctg 1390
gcctttactg gatcccaaaa gcatttaagg tacatgttcc aaaaactttg aaaagctaaa 1450
tggtttcccat gatcgctcat tcttctttta tgattcatac gttattcctt ataaagtaag 1510
aactttgttt tctctctatc aaggcagcta ttttattaaa tttttcactt agtctgagaa 1570
atagcagata gtctcatatt taggaaaact ttccaaataa aataaatgtt attctctgat 1630
aaagagctaa tacagaaatg ttcaagttat tttactttct ggtaatgtct tcagtaaaat 1690
attttcttta tctaaatatt aacattctaa gtctaccaaa aaaagtttta aactcaagca 1750
ggccaaaacc aatatgctta taagaaataa tgaaaagttc atccatttct gataaagttc 1810
tctatggcaa agtctttcaa atacgagata actgcaaaat attttccttt tatactacag 1870
aaatgagaat ctcatcaata aattagttca agcataagat gaaaacagaa tattctgtgg 1930
tgccagtgca cactaccttc ccaccatac acatccatgt tcaactgtaac aaactgaata 1990
ttcaciaa      1997

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<210> 22  
 <211> 298  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..19

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<400> 22
Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Leu Val Pro Leu
          -15          -10          -5
Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile Tyr Asp
          1          5          10
Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp Tyr Glu
          15          20          25
Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
          30          35          40          45
Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr
          50          55          60
Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu
          65          70          75
Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp

```

```

      80              85              90
Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe
  95              100              105
Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile Pro Asn
110              115              120              125
Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile Glu Asp
      130              135              140
Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu
      145              150              155
Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe
      160              165              170
Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala
      175              180              185
Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala
190              195              200              205
Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His
      210              215              220
Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys
      225              230              235
Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu
      240              245              250
Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe Ile Cys
      255              260              265
Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe
270              275

```

```

<210> 23
<211> 1746
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..9

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```

<220>
<221> CDS
<222> 10..1212

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```

<220>
<221> 3'UTR
<222> 1213..1746

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<220>
<221> polyA_signal
<222> 1709..1714

```

```

<220>
<221> polyA_site
<222> 1733..1746

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```

<400> 23
gcctcacca atg gtt ccc ttc atc tat ctg caa gcc cac ttt aca ctc tgt    51
      Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys
      -15              -10              -5

```

tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg	99
Ser Gly Trp Ser Ser Thr Arg Asp Leu Arg Lys Gly Val Tyr Val	
1 5 10	
ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta	147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val	
15 20 25 30	
agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc	195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala	
35 40 45	
atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc	243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly	
50 55 60	
atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg	291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro	
65 70 75	
gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc	339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu	
80 85 90	
ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa	387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu	
95 100 105 110	
gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac	435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His	
115 120 125	
tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg	483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp	
130 135 140	
tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg	531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu	
145 150 155	
aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt	579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser	
160 165 170	
ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc	627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val	
175 180 185 190	
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc	675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe	
195 200 205	
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg	723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp	
210 215 220	
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac	771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn	
225 230 235	
cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg	819
Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val	
240 245 250	
gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca	867
Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser	
255 260 265 270	
cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc	915
Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe	
275 280 285	
tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc	963

```

Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
      290      295      300
gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc cct 1011
Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
      305      310      315
ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca cag aca 1059
Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
      320      325      330
gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc 1107
Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
      335      340      345      350
gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg cgc tgc 1155
Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
      355      360      365
ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc 1203
Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser
      370      375      380
ctg ctg aag tgaggaggcc catgggcaga agatagggat tcccctggac 1252
Leu Leu Lys
      385
cacacctccg tggttcactt tggtcacaag taggagacac agatggcacc tgtggccaga 1312
gcacctcagg accctcccca cccaccaaat gcctctgcct tgatggagaa ggaaaaggct 1372
ggcaaggtgg gttccagga ctgtacctgt aggagacaga aaagagaaga aagaagcact 1432
ctgctggcgg gaatactctt ggtcacctca aatttaagtc gggaaattct gctgcttgaa 1492
acttcagccc tgaacctttg tcaccattcc tttaaattct ccaacccaaa gtattcttct 1552
tttcttagtt tcagaagtac tggcatcaca cgcaggttac cttggcgtgt gtccctgtgg 1612
taccctggca gagaagagac caagcttggt tccctgctgg ccaaagtcag taggagagga 1672
tgcacagttt gctatttgct ttagagacag ggactgtata aacaagccta acattggtgc 1732
aaaaaaaaaa aaaa 1746

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<210> 24
<211> 401
<212> PRT
<213> Homo sapiens

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```

<220>
<221> SIGNAL
<222> 1..17

```

```

<400> 24
Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys Ser Gly
      -15      -10      -5
Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
      1      5      10      15
Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
      20      25      30
Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
      35      40      45
Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
      50      55      60
Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro Glu Pro
      65      70      75
Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser
      80      85      90      95
Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu

```

```

      100      105      110
Ala Ser Val Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu
      115      120      125
Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr
      130      135      140
Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met
      145      150      155
Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr
160      165      170      175
Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser
      180      185      190
Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu
      195      200      205
Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile
      210      215      220
Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser
      225      230      235
Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp
240      245      250      255
Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser
      260      265      270
Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val
      275      280      285
Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys
      290      295      300
His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val
      305      310      315
Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
320      325      330      335
Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu
      340      345      350
Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg
      355      360      365
Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu
      370      375      380

```

Lys

<210> 25  
 <211> 1239  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..126

<220>  
 <221> CDS  
 <222> 127..879

<220>  
 <221> 3'UTR  
 <222> 880..1239

<220>



&lt;221&gt; polyA\_site

&lt;222&gt; 1224..1239

&lt;400&gt; 25

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agtctaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg      60
gccaggagag tcccgacagg agtgtcaggt ttcaatctca gcaccagcca ctgagagcag    120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
            -20                      -15                      -10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca      216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
            -5                      1                      5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca      264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
            10                      15                      20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
            25                      30                      35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
            40                      45                      50                      55
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
            60                      65                      70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg      456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
            75                      80                      85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc      504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
            90                      95                      100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag      552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
            105                      110                      115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg      600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
            120                      125                      130                      135
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca      648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
            140                      145                      150
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg      696
Arg Arg His Thr Arg Ser Ala Glu Asp Ser Glu Arg Asp Pro Leu
            155                      160                      165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt      744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
            170                      175                      180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
            185                      190                      195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
            200                      205                      210                      215
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgct      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
            220                      225
ggaagggcac cctctttaac ccacccctca gcaaacgcag ctcttcccaa ggaccaggtc  949

```

```

ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct 1009
gggggtccctt ccacaggagg tcctgtgaga accaaccttt gagggccaag tcatgggggtt 1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa 1129
ctagaaattt ccccttcatg aaggtagaga gaaggggtct ctcccaacat atttctcttc 1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa 1239

```

```

<210> 26
<211> 251
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..24

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<400> 26
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
          -20          -15          -10
Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
          -5          1          5
Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
  10          15          20
Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
  25          30          35          40
Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
          45          50          55
Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
          60          65          70
Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
          75          80          85
Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
          90          95          100
Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
  105          110          115          120
Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
          125          130          135
Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
          140          145          150
His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
          155          160          165
Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
          170          175          180
Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
  185          190          195          200
Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
          205          210          215
Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
          220          225

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```

<210> 27
<211> 1179
<212> DNA
<213> Homo sapiens

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<220>

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<221> 5'UTR  
<222> 1..115

<220>  
<221> CDS  
<222> 116..961

<220>  
<221> 3'UTR  
<222> 962..1179

<220>  
<221> polyA\_signal  
<222> 1145..1150

<220>  
<221> polyA\_site  
<222> 1164..1179

<220>  
<221> MISC\_FEATURE  
<222> 116  
<223> Xaa = Asn,Thr

<220>  
<221> MISC\_FEATURE  
<222> 233  
<223> Xaa = Phe,Ser

<400> 27  
acaaattccc aatgcagtta caggatcctg ggaagcagag tgtctggatg gaacctgagc 60  
tgggtctctg actcacttct gacttttaggc gtcgaggac tgtgcccagg agcag atg 118  
Met  
1  
cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa 166  
Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln  
5 10 15  
cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt 214  
Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu  
20 25 30  
gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag 262  
Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln  
35 40 45  
tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga 310  
Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly  
50 55 60 65  
ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat 358  
Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr  
70 75 80  
tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct 406  
Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser  
85 90 95  
gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc 454  
Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly  
100 105 110

```

ttt gga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa      502
Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys
115                               120                               125
aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac      550
Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp
130                               135                               140                               145
ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc      598
Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe
150                               155                               160
aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat      646
Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr
165                               170                               175
tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg      694
Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val
180                               185                               190
cag tgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga      742
Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg
195                               200                               205
gat cat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc      790
Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly
210                               215                               220                               225
tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac      838
Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr
230                               235                               240
agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc      886
Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr
245                               250                               255
tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg      934
Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg
260                               265                               270
cca aat gat ttt att cca aat gta att taattgctgc tgttgggctt      981
Pro Asn Asp Phe Ile Pro Asn Val Ile
275                               280
tcgtttctgc aattcagctt tgtttaaagt gatttgaaaa atactcattc tgaacatadc 1041
catgcgcaat catgataact gttgtgagta gtgcttttca ttcttctcac ttgcctttgt 1101
tacttaatgt gctttcagta cagcagatat gcaatattca ccaaataaat gtagactgtg 1161
tcaaaaaaaaa aaaaaaaaaa 1179

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<210> 28  
 <211> 282  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MISC\_FEATURE  
 <222> 116  
 <223> Xaa = Asn,Thr

<220>  
 <221> MISC\_FEATURE  
 <222> 233  
 <223> Xaa = Phe,Ser

<400> 28  
 Met Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln

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1           5           10           15
Gln Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe
20
Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg
35
Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser
50
Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val
65
Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg
85
Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn
100
Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn
115
Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile
130
Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn
145
Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu
165
Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
180
Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
195
Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
210
Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
225
Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
245
Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
260
Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
275
280

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```

<210> 29
<211> 1118
<212> DNA
<213> Homo sapiens

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```

<220>
<221> 5'UTR
<222> 1..344

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```

<220>
<221> CDS
<222> 345..1118

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<220>
<221> polyA_site
<222> 1103..1118

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<220>
<221> MISC_FEATURE

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&lt;222&gt; 30

&lt;223&gt; Xaa = Glu, \*

&lt;400&gt; 29

```

aatcctagtc ttcgtttggg cccggttgac tcttcctata gcccagaggg cgagagggcc 60
tgtggcctgg ggggaaggagg acgaggttct gcctggatcc cagcaggacg ctgtgccatt 120
tgggaacaaa ggaatagtct gcctggaatc cctgcagatc ttggggccgg aggccagtc 180
aacccttggg gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
cgccccgcag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
                                Met Gly Arg Thr
cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
-15 -10 -5 1
tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
5 10 15
atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
20 25 30
gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
35 40 45
aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu
50 55 60 65
gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc 644
Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser
70 75 80
gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag 692
Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys
85 90 95
gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc 740
Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile
100 105 110
tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg 788
Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg
115 120 125
ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg 836
Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg
130 135 140 145
gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct 884
Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala
150 155 160
cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat 932
Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr
165 170 175
aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac 980
Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn
180 185 190
atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc 1028
Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val
195 200 205
act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt 1076
Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg

```



<211> 1273  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..13

<220>  
 <221> CDS  
 <222> 14..1048

<220>  
 <221> 3'UTR  
 <222> 1049..1273

<220>  
 <221> polyA\_signal  
 <222> 1234..1239

<220>  
 <221> polyA\_site  
 <222> 1258..1273

<400> 31  
 agaggttggg aag atg gcg tgg cga ggc tgg gcg cag aga ggc tgg ggc 49  
                   Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly  
                   -25                  -20                  -15  
 tgc ggc cag gcg tgg ggt gcg tcg gtg ggc ggc cgc agc tgc gag gag 97  
 Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu  
                   -10                  -5                  1  
 ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac 145  
 Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn  
                   5                  10                  15  
 ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt 193  
 Phe Phe Ile Gln Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val  
 20                  25                  30                  35  
 gaa cct cga aga tca gac cca ggg aca agt ggt gaa gca tac aag aga 241  
 Glu Pro Arg Arg Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg  
                   40                  45                  50  
 agt gct ttg att cct cct gtg gaa gaa aca gtc ttt tat cct tct ccc 289  
 Ser Ala Leu Ile Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro  
                   55                  60                  65  
 tat cct ata agg agt ctc ata aaa cct tta ttt ttt act gtt ggg ttt 337  
 Tyr Pro Ile Arg Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe  
                   70                  75                  80  
 aca ggc tgt gca ttt gga tca gct gct att tgg caa tat gaa tca ctg 385  
 Thr Gly Cys Ala Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu  
                   85                  90                  95  
 aaa tcc agg gtc cag agt tat ttt gat ggt ata aaa gct gat tgg ttg 433  
 Lys Ser Arg Val Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu  
 100                  105                  110                  115  
 gat agc ata aga cca caa aaa gaa gga gac ttc aga aag gag att aac 481  
 Asp Ser Ile Arg Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn  
                   120                  125                  130



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aag tgg tgg aat aac cta agt gat ggc cag cgg act gtg aca ggt att 529
Lys Trp Trp Asn Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile
      135      140      145
ata gct gca aat gtc ctt gta ttc tgt tta tgg aga gta cct tct ctg 577
Ile Ala Ala Asn Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu
      150      155      160
cag cgg aca atg atc aga tat ttc aca tcg aat cca gcc tca aag gtc 625
Gln Arg Thr Met Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val
      165      170      175
ctt tgt tct cca atg ttg ctg tca aca ttc agt cat ttc tcc tta ttt 673
Leu Cys Ser Pro Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe
      180      185      190      195
cac atg gca gca aat atg tat gtt ttg tgg agc ttc tct tcc agc ata 721
His Met Ala Ala Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile
      200      205      210
gtg aac att ctg ggt caa gag cag ttc atg gca gtg tac cta tct gca 769
Val Asn Ile Leu Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala
      215      220      225
ggg gtt att tcc aat ttt gtc agt tac gtg ggt aaa gtt gcc aca gga 817
Gly Val Ile Ser Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly
      230      235      240
aga tat gga cca tca ctt ggt gca gcc ctg aaa gcc att atc gcc atg 865
Arg Tyr Gly Pro Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met
      245      250      255
gat aca gca gga atg atc ctg gga tgg aaa ttt ttt gat cat gcg gca 913
Asp Thr Ala Gly Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala
      260      265      270      275
cat ctt ggg gga gct ctt ttt gga ata tgg tat gtt act tac ggt cat 961
His Leu Gly Gly Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His
      280      285      290
gaa ctg att tgg aag aac agg gag ccg cta gtg aaa atc tgg cat gaa 1009
Glu Leu Ile Trp Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu
      295      300      305
ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaactggg 1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys
      310      315      320
attggacagt agtgggtgcat ctggctccttg ccgcctgaga gccccaggag acatcggcta 1118
gagtgaccat ggctatgctc ccgtctggaa gatgccagca tctggcctcc cacttttttc 1178
agctgtgtcc cccagtcctg gtcttttttag aatgtgaatg atgataaagt tgtgaaataa 1238
aggtttctat ctagtttgca aaaaaaaaaa aaaaa 1273

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<210> 32  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..26

<400> 32  
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala  
 -25 -20 -15  
 Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val  
 -10 -5 1 5

```

Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
      10      15      20
Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
      25      30      35
Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
      40      45      50
Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
      55      60      65      70
Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
      75      80      85
Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
      90      95      100
Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
      105      110      115
Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
      120      125      130
Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
      135      140      145      150
Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
      155      160      165
Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
      170      175      180
Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
      185      190      195
Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
      200      205      210
Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
      215      220      225      230
Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
      235      240      245
Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
      250      255      260
Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
      265      270      275
Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
      280      285      290
Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
      295      300      305      310
Gly Pro Lys Lys Gly Gly Ser Lys
      315

```

```

<210> 33
<211> 723
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..72

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```

<220>
<221> CDS
<222> 73..672

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```

<220>

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<221> 3'UTR  
<222> 673..723

<220>  
<221> polyA\_signal  
<222> 689..694

<220>  
<221> polyA\_site  
<222> 708..723

<400> 33  
acaagaaaag aacatgggtct agactgaagt accaactaaa tcattctcctt tcaaattatc 60  
accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111  
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val  
1 5 10  
ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159  
Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser  
15 20 25  
gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207  
Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg  
30 35 40 45  
aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255  
Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr  
50 55 60  
ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303  
Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro  
65 70 75  
agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351  
Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val  
80 85 90  
ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399  
Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr  
95 100 105  
aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447  
Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala  
110 115 120 125  
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495  
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu  
130 135 140  
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543  
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys  
145 150 155  
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591  
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe  
160 165 170  
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639  
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys  
175 180 185  
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692  
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys  
190 195 200  
aagatgtgtt aaaataaaaa aaaaaaaaaa t 723

<210> 34

<211> 200  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro  
 1 5 10 15  
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr  
 20 25 30  
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys  
 35 40 45  
 Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe  
 50 55 60  
 Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro  
 65 70 75 80  
 Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile  
 85 90 95  
 Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr  
 100 105 110  
 Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala  
 115 120 125  
 Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn  
 130 135 140  
 Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr  
 145 150 155 160  
 Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile  
 165 170 175  
 Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu  
 180 185 190  
 Asp Cys Asp Cys Glu Gln Cys Cys  
 195 200

<210> 35  
 <211> 845  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..118

<220>  
 <221> CDS  
 <222> 119..655

<220>  
 <221> 3'UTR  
 <222> 656..845

<220>  
 <221> polyA\_signal  
 <222> 809..814

<220>  
 <221> polyA\_site

&lt;222&gt; 830..845

&lt;400&gt; 35

```

acaaatagcc ccgatatct gtgttaccag ccttgtctcg gccacctcaa ggataatcac 60
taaattctgc caaaaggact gaggaacggg gcctggaaaaa gggcaagaat atcacggc 118
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctg ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctg ttc cat aac ctg ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
tcc ctg acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tgc ttc ttc atc ctg ctg ctg att atc ctg ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctg ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
Gly Pro Tyr
atttatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggg 755
attatctctc tatcagataa gattttgtta atgtactatt ttactcttca ataaataaaa 815
cagtttatta tcgcaaaaaa aaaaaaaaaa 845

```

&lt;210&gt; 36

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

```

Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro

```

```

      35              40              45
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
   50              55              60
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
   65              70              75              80
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
              85              90              95
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
      100              105              110
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
      115              120              125
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
      130              135              140
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
      145              150              155              160
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
              165              170              175
Gly Pro Tyr

```

```

<210> 37
<211> 517
<212> DNA
<213> Homo sapiens

```

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<220>
<221> 5'UTR
<222> 1..16

```

```

<220>
<221> CDS
<222> 17..259

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```

<220>
<221> 3'UTR
<222> 260..517

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<400> 37
ttccatagaa tgggag atg tca cca ggg cag cct atg aca ttc ccc cca gag 52
      Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu
              1              5              10
gcc ctg tgg gtg acc gtg ggg ctg tct gtc tgt ctc att gca ctg ctg 100
Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu
      15              20              25
gtg gcc ctg gct ttc gtg tgc tgg aga aag atc aaa cag agc tgt gag 148
Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu
      30              35              40
gag gag aat gca gga gct gag gac cag gat ggg gag gga gaa ggc tcc 196
Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser
      45              50              55              60
aag aca gcc ctg cag cct ctg aaa cac tct gac agc aaa gaa gat gat 244
Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp
              65              70              75
gga caa gaa ata gcc tgaccatgag gaccagggag ctgctacccc tccctacagc 299
Gly Gln Glu Ile Ala
      80

```

```

tcctaccctc tggctgcaat ggggctgcac tgtgagccct gcccccaaca gatgcaccc 359
gctctgacag gtgggctcct tctccaaagg atgcgataca cagaccactg tgcagcctta 419
tttctccaat ggacatgatt cccaagtcat cctgctgcct tttttcttat agacacaatg 479
aacagaccac ccacaacctt agttctctaa gtcaccc 517

```

```

<210> 38
<211> 81
<212> PRT
<213> Homo sapiens

```

```

<400> 38
Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val
1          5          10          15
Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
          20          25          30
Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala
          35          40          45
Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
          50          55          60
Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
65          70          75          80
Ala

```

```

<210> 39
<211> 1816
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..259

```

```

<220>
<221> CDS
<222> 260..1048

```

```

<220>
<221> 3'UTR
<222> 1049..1816

```

```

<220>
<221> polyA_signal
<222> 1782..1787

```

```

<220>
<221> polyA_site
<222> 1801..1816

```

```

<400> 39
actctggggc cattgccagc cggctgtagg cattcagggc agtgtcttct gcattctccta 60
ggaacctcg gagcggcagc tccgggcgct ggtagcgaga ggcgggttcc ggagatccc 120
gcctcacttc gtccactgt ggtaggggt gagtcctgcg aatgttaagt gatttgctca 180
aggtgcccac ttcgcaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu

```

```

                                -15                                -10
ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg      340
Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
                                -5                                5
atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg      388
Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
                                10                                15                                20
ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat      436
Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
25                                30                                35                                40
gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tcg tgg gtg ggg ccc      484
Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro
                                45                                50                                55
aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc      532
Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe
                                60                                65                                70
gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat      580
Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His
                                75                                80                                85
gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc acc      628
Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr
                                90                                95                                100
act gtc ttc ctc ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc      676
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe
105                                110                                115                                120
ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct atc      724
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile
                                125                                130                                135
cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc gtc      772
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val
                                140                                145                                150
att tcg ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc      820
Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr
                                155                                160                                165
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc      868
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr
                                170                                175                                180
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt ctg      916
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu
185                                190                                195                                200
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag      964
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln
                                205                                210                                215
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac      1012
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr
                                220                                225                                230
gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgtc      1058
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp
                                235                                240
tcccaagaac agagcctgtc cccagatgtc ccagtagcga tgagtaacag aggtggctgt 1118
ggacttcttc tacttctcct tgcctgatca gggccttctc gcctcccgtc gggcaggtct 1178
ggccttgtc tcttgccagg gccccagccc ctctgaccac tctgcagctc accatgcagc 1238
tgatgcaaaa gttgtggtgt ccagtgtgca gcagccctgg gagccactgc caccttcaga 1298
gggggttcctt gctgagaccc acattgcttc acctggcccc accatggctg cttgcctggc 1358
ccaacctagc gttctgtgcc atgctagaac ttgagctggt gctcttcttc aggggaggaa 1418

```



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ataggggtgga gagcgggaag ggtcttgctc ctaagtgttg ctgctgtggc ttttttgctt 1478
tctccaaaga cgcactgccg ggtcccaagc ttcagactgc tgtgcttagt aagcaagtga 1538
gaagcctggg gtttgagacc cacctactct ctggcagcat cagcatccta ctctggcaa 1598
catcaggcca acgtccaccc cagcctcaca ttgccagatg ttggcagaag ggctaattatt 1658
gaccgtcttg actggctgga gccttcaaag ccactgggat gtcctccagg cacctggggtc 1718
ccatgaccag ctcccgtct ccataggggt aggcatttca ctggtttatg aagctcgagt 1778
ttcattaat atgttaagaa tcaaaaaaaaa aaaaaaaaa 1816

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<210> 40
<211> 263
<212> PRT
<213> Homo sapiens

```

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<220>
<221> SIGNAL
<222> 1..20

```

```

<400> 40
Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu Leu Gly Ser Leu
-20          -15          -10          -5
Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp Met Gln Tyr Trp Arg
          1          5          10
Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
          15          20          25
Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
          30          35          40
Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys
45          50          55          60
Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val
          65          70          75
Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn
          80          85          90
Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe
          95          100          105
Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
          110          115          120
Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly
125          130          135          140
Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn
          145          150          155
Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser
          160          165          170
Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val
          175          180          185
Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys
          190          195          200
Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Leu Gln Leu
205          210          215          220
Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly
          225          230          235
Arg Gln Pro Tyr Lys Ser Trp
          240

```

```

<210> 41
<211> 643

```

<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> 1..90

<220>  
<221> CDS  
<222> 91..462

<220>  
<221> 3'UTR  
<222> 463..643

<220>  
<221> polyA\_signal  
<222> 607..612

<220>  
<221> polyA\_site  
<222> 628..643

<400> 41  
accctacc cagccccct cccgcgcgcg cggtaaata cccgcacctg agcatcggct 60  
cacacctgca cccgcgccgg gcatagcacc atg cct gct tgt cgc cta ggc ccg 114  
Met Pro Ala Cys Arg Leu Gly Pro  
-25  
cta gcc gcc gcc ctc ctc ctc agc ctg ctg ctg ttc ggc ttc acc cta 162  
Leu Ala Ala Ala Leu Leu Leu Ser Leu Leu Leu Phe Gly Phe Thr Leu  
-20 -15 -10  
gtc tca ggc aca gga gca gag aag act ggc gtg tgc ccc gag ctc cag 210  
Val Ser Gly Thr Gly Ala Glu Lys Thr Gly Val Cys Pro Glu Leu Gln  
-5 1 5 10  
gct gac cag aac tgc acg caa gag tgc gtc tcg gac agc gaa tgc gcc 258  
Ala Asp Gln Asn Cys Thr Gln Glu Cys Val Ser Asp Ser Glu Cys Ala  
15 20 25  
gac aac ctc aag tgc tgc agc gcg ggc tgt gcc acc ttc tgc tct ctg 306  
Asp Asn Leu Lys Cys Cys Ser Ala Gly Cys Ala Thr Phe Cys Ser Leu  
30 35 40  
ccc aat gat aag gag ggt tcc tgc ccc cag gtg aac att aac ttt ccc 354  
Pro Asn Asp Lys Glu Gly Ser Cys Pro Gln Val Asn Ile Asn Phe Pro  
45 50 55  
cag ctc ggc ctc tgt cgg gac cag tgc cag gtg gac agc cag tgt cct 402  
Gln Leu Gly Leu Cys Arg Asp Gln Cys Gln Val Asp Ser Gln Cys Pro  
60 65 70 75  
ggc cag atg aaa tgc tgc cgc aat ggc tgt ggg aag gtg tcc tgt gtc 450  
Gly Gln Met Lys Cys Cys Arg Asn Gly Cys Gly Lys Val Ser Cys Val  
80 85 90  
act ccc aat ttc tgagctccag ccaccaccag gctgagcagt gaggagagaa 502  
Thr Pro Asn Phe  
95  
agttttctgcc tggccctgca tctggttcca gccacactgc cctccccctt ttcgggactc 562  
tgtattccct cttgggctga ccacagcttc tccctttccc aaccaataaa gtaaccactt 622  
tcagcaaaaa aaaaaaaaaa a 643

<210> 42  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..30

<400> 42  
 Met Pro Ala Cys Arg Leu Gly Pro Leu Ala Ala Ala Leu Leu Leu Ser  
 -30 -25 -20 -15  
 Leu Leu Leu Phe Gly Phe Thr Leu Val Ser Gly Thr Gly Ala Glu Lys  
 -10 -5 1  
 Thr Gly Val Cys Pro Glu Leu Gln Ala Asp Gln Asn Cys Thr Gln Glu  
 5 10 15  
 Cys Val Ser Asp Ser Glu Cys Ala Asp Asn Leu Lys Cys Cys Ser Ala  
 20 25 30  
 Gly Cys Ala Thr Phe Cys Ser Leu Pro Asn Asp Lys Glu Gly Ser Cys  
 35 40 45 50  
 Pro Gln Val Asn Ile Asn Phe Pro Gln Leu Gly Leu Cys Arg Asp Gln  
 55 60 65  
 Cys Gln Val Asp Ser Gln Cys Pro Gly Gln Met Lys Cys Cys Arg Asn  
 70 75 80  
 Gly Cys Gly Lys Val Ser Cys Val Thr Pro Asn Phe  
 85 90

<210> 43  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..227

<220>  
 <221> CDS  
 <222> 228..500

<400> 43  
 actcttactc tttctctctc actctctctc ttttcccacc cttaagccaa gtacagggat 60  
 agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120  
 ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180  
 ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236  
 Met Gln Gly  
 -30  
 act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284  
 Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg  
 -25 -20 -15  
 aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332  
 Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met  
 -10 -5 1  
 aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380

```

Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
  5              10              15
cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
20              25              30              35
gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
              40              45              50
gtt cct ttc tcc gaa ctg aaa gac a 501
Val Pro Phe Ser Glu Leu Lys Asp
              55

```

```

<210> 44
<211> 91
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..33

```

```

<400> 44
Met Gln Gly Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val
      -30              -25              -20
Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Leu
      -15              -10              -5
Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
  1              5              10              15
Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
      20              25              30
Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
      35              40              45
Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
      50              55

```

```

<210> 45
<211> 960
<212> DNA
<213> Homo sapiens

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```

<220>
<221> 5'UTR
<222> 1..97

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```

<220>
<221> CDS
<222> 98..934

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<220>
<221> 3'UTR
<222> 935..960

```

```

<400> 45
ataatcacct ctcattccag actatgttag gtcttaatgg tgggaggacg cccgagtgt 60
cggccccgttt caccgccgagg aggaaggaca ctggggtc atg acg cca tca gaa ggc 115

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J:\GEN\091.US05.DIV\Sequence\SEOLIST-corr-w-hdr-ftp.doc/DNB\jai

<210> 46  
 <211> 279  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu  
 1 5 10 15  
 Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val Leu Leu Arg Asp  
 20 25 30  
 Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys  
 35 40 45  
 Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser  
 50 55 60  
 Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu  
 65 70 75 80  
 Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu  
 85 90 95  
 Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys  
 100 105 110  
 Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp  
 115 120 125  
 Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala  
 130 135 140  
 Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys  
 145 150 155 160  
 Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro  
 165 170 175  
 Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly  
 180 185 190  
 Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln  
 195 200 205  
 Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser  
 210 215 220  
 Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp  
 225 230 235 240  
 Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys  
 245 250 255  
 Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly  
 260 265 270  
 Trp Gly Trp Gly Gln Gly Phe  
 275

<210> 47  
 <211> 1294  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..266

<220>  
 <221> CDS

<222> 267..1139

<220>

<221> 3'UTR

<222> 1140..1294

<220>

<221> polyA\_signal

<222> 1246..1251

<220>

<221> polyA\_site

<222> 1279..1294

<400> 47

```

gactctgagg ctccctcttt gctctaacag acagcagcga ctttaggctg gataatagtc 60
aaattctttac ctgctcttt cactgctagt aagatcagat tgcgtttctt tcagttactc 120
ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
ttcaatacct ggaaggaaaa acaaaataac ctcaactccg ttttgaaaaa aacattccaa 240
gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
                Met Ile Tyr Thr Met Lys Lys Val His
                -25                                -20

gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
Ala Leu Trp Ala Ser Val Cys Leu Leu Asn Leu Ala Pro Ala Pro
                -15                                -10                                -5

ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
                1                                5                                10

acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
15                                20                                25                                30

gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
35                                40                                45

att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
50                                55                                60

aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
65                                70                                75

aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
80                                85                                90

cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
95                                100                                105                                110

gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu
115                                120                                125

aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773
Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe
130                                135                                140

cag gtg gat aat tat gga acc cag ctc aat gct gtg aat aac tcc ctg 821
Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn Ala Val Asn Asn Ser Leu
145                                150                                155

```

```

act ccg caa tca acc aag gtt ccc agc ctt ttt gaa ttt cac ggt ccc      869
Thr Pro Gln Ser Thr Lys Val Pro Ser Leu Phe Glu Phe His Gly Pro
    160                      165                      170
tca tgg tgt ctc act cca gca gac aga gga ttg tgt cgt gcc aat gag      917
Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu
    175                      180                      185                      190
aac aga ttc tac tac aat tca gtc att ggg aaa tgc cgc cca ttt aag      965
Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly Lys Cys Arg Pro Phe Lys
                      195                      200                      205
tac agt gga tgt ggg gga aat gaa aac aat ttt act tcc aaa caa gaa      1013
Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu
                      210                      215                      220
tgt ctg agg gca tgt aaa aaa ggt ttc atc caa aga ata tca aaa gga      1061
Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly
                      225                      230                      235
ggc cta att aaa acc aaa aga aaa aga aag aag cag aga gtg aaa ata      1109
Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys Lys Gln Arg Val Lys Ile
                      240                      245                      250
gca tat gaa gaa att ttt gtt aaa aat atg tgaatttggt atagcaatgt      1159
Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
    255                      260
aacattaatt ctactaaata ttttatatga aatgtttcac tatgattttc tattttttctt 1219
ctaaaatgct ttttaattaat atgttcatta aattttctat gcttattgta cttgtttacca 1279
aaaaaaaaaaaa aaaaaa                                         1294

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```

<210> 48
<211> 291
<212> PRT
<213> Homo sapiens

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```

<220>
<221> SIGNAL
<222> 1..28

```

```

<400> 48
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
    -25                      -20                      -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
    -10                      -5                      1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
    5                      10                      15                      20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
    25                      30                      35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
    40                      45                      50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
    55                      60                      65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
    70                      75                      80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
    85                      90                      95                      100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
    105                      110                      115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
    120                      125                      130

```



```

Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
      135      140      145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
      150      155      160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165      170      175      180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
      185      190      195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
      200      205      210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
      215      220      225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
      230      235      240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245      250      255      260
Lys Asn Met

```

```

<210> 49
<211> 1194
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..47

```

```

<220>
<221> CDS
<222> 48..1100

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<220>
<221> 3'UTR
<222> 1101..1194

```

```

<220>
<221> polyA_signal
<222> 1159..1164

```

```

<220>
<221> polyA_site
<222> 1179..1194

```

```

<400> 49
ctcctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct      56
                                   Met Pro Ser
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc      104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20      -15      -10      -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag      152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
      1      5      10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa      200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
      15      20      25

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ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
30 35 40
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu
45 50 55 60
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc 344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala
65 70 75
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac 392
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn
80 85 90
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag 440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys
95 100 105
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt 488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe
110 115 120
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag 536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu
125 130 135 140
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag 584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys
145 150 155
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg 632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp
160 165 170
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg 680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu
175 180 185
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat 728
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp
190 195 200
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta 776
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu
205 210 215 220
cat tta ccc aaa ctg tcc att act gga acc tat gat ctg aag agc gtc 824
His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val
225 230 235
ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg gct gac ctc 872
Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu
240 245 250
tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag gcc gtg cat 920
Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His
255 260 265
aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct gct ggg gcc 968
Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
270 275 280
atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag gtc aag ttc 1016
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe
285 290 295 300
aac aaa ccc ttt gtc ttc tta atg att gac caa aat acc aag tct ccc 1064
Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr Lys Ser Pro
305 310 315
ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa taactgcctc 1110

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Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys

320

325

tgcgtcctca acccctcccc tccatccctg gccccctccc tggatgacat taaagaagg 1170

ttgagctgaa aaaaaaaaaa aaaa

1194

<210> 50

<211> 351

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..24

<400> 50

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-20

-15

-10

Cys Leu Val Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu

-5

1

5

Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln

10

15

20

Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp

25

30

35

40

Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly

45

50

55

Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His

60

65

70

Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys

75

80

85

Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp

90

95

100

Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr

105

110

115

120

Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr

125

130

135

Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro

140

145

150

Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu

155

160

165

Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile

170

175

180

Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu

185

190

195

200

Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser

205

210

215

Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu

220

225

230

Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly

235

240

245

Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys

250

255

260

Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala

265

270

275

280

Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu

285

290

295

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cgacttttagg ctggataata gtcaaattct tacctcgctc ttctactgct agtaagatca	120
gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag	180
aagtagagaa gataaatcct gtcttcaata cctggaagga aaaacaaaat aacctcaact	240
ccgtttttgaa aaaaacattc caagaacttt catcagagat tttacttag atg att tac	298
	Met Ile Tyr
	-25
aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt	346
Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu	
	-20 -15 -10
aat ctt gcc cct gcc cct ctt aat gct gat tct gag gaa gat gaa gaa	394
Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu	
	-5 1 5
cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat	442
His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys Leu Met His	
	10 15 20
tca ttt tgt gca ttc aag tcg gat gat ggc cca tgt aaa gca atc atg	490
Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys Ala Ile Met	
	25 30 35 40
aaa aga ttt ttc ttc aat att ttc act cga cag tgc gaa gaa ttt ata	538
Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile	
	45 50 55
tat ggg gga tgt gaa gga aat cag aat cga ttt gaa agt ctg gaa gag	586
Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu	

60	65	70	
tgc aaa atg tgt aca aga gaa aag cca gat ttc tgc ttt ttg gaa	634		
Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu			
75	80	85	
gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat aac	682		
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn			
90	95	100	
aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga tgc ctg ggc	730		
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly			
105	110	115	120
aat atg aac aat ttt gag aca ctg gaa gaa tgc aag aac att tgt gaa	778		
Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu			
125	130	135	
gat ggt ccg aat ggt ttc cag gtg gat aat tat gga acc cag ctg aat	826		
Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn			
140	145	150	
gct gtg aat aac tcc ctg act ccg caa tca acc aag gtt ccc agc ctt	874		
Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu			
155	160	165	
ttt gaa ttt cac ggt ccc tca tgg tgt ctc act cca gca gac aga gga	922		
Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly			
170	175	180	
ttg tgt cgt gcc aat gag aac aga ttc tac tac aat tca gtc att ggg	970		
Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly			
185	190	195	200
aaa tgc cgc cca ttt aag tac agt gga tgt ggg gga aat gaa aac aat	1018		
Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn			
205	210	215	
ttt act tcc aaa caa gaa tgt ctg agg gca tgt aaa aaa ggt ttc atc	1066		
Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile			
220	225	230	
caa aga ata tca aaa gga ggc cta att aaa acc aaa aga aaa aga aag	1114		
Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys			
235	240	245	
aag cag aga gtg aaa ata gca tat gaa gaa att ttt gtt aaa aat atg	1162		
Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met			
250	255	260	
tgaatttggt atagcaatgt aacattaatt ctactaaata ttttatatga aatgtttcac	1222		
tatgattttc tattttttctt ctaaaatgct tttaattaat atgttcatta aattttctat	1282		
gcttatttga cttgttatca aaaaaaaaaa aaaaa	1317		

&lt;210&gt; 52

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; 1..28

&lt;400&gt; 52

Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys

-25

-20

-15

Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu

-10

-5

1

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Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5      10      15      20
Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
      25      30      35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
      40      45      50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
      55      60      65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
      70      75      80
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
85      90      95      100
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
      105      110      115
Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
      120      125      130
Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
      135      140      145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
      150      155      160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165      170      175      180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
      185      190      195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
      200      205      210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
      215      220      225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
      230      235      240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245      250      255      260
Lys Asn Met

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<210> 53
<211> 1907
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..1043

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<220>
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<222> 1044..1664

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<220>
<221> 3'UTR
<222> 1665..1907

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<220>
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<222> 1869..1874

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&lt;220&gt;

&lt;221&gt; polyA\_site

&lt;222&gt; 1892..1907

&lt;400&gt; 53

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caaaaaaatt ctaggtcatg atccccataa atgaagagtg atcagtccaa tcccaggga 60
cctggacatt ttgggtattg tttcagtgga acatgccttt cataagttcc attttcttgg 120
gtatctctta ggaagcaagc ataggaaaca ggcccatccg tctgcctgtt ttgcttcctc 180
atctcacttc tacacgaggg tgctgtgct caattgctgt tttcccctaa agagactctt 240
ttccataagt ttgtgaaatg ccatcgacaa acctgatcgc attgcatttc actctgctgt 300
tgagtcgatt tttcttttatt ttatcattta gtaactcctt gctctacaga gctttcacct 360
tccacatatt tcagattcat tctttcctaa actatgtggg ggtctacgtc ctcaactgact 420
tatcaacatg ctaccatcat gcacttctta tctctattcc tcttctttaa atttgggttc 480
aaatggctca caccattatt ctgagctatt acctgcctac gcagtcctag aaagtaagt 540
attcaggaaa cattcccca aagtaaagtt tctcaggtta gatcagaaga ctcccatgag 600
tcaactgctg tcaggatcac atctggctcc ttgaagagtg attcatcaga ccttacatag 660
atcttgtcat aaaaatgaaa gaggcctcgg gggaaggtct tgggctgggt gcttctgttg 720
gagtcctggg ctgtgggggt aaagccgtgg ctgtagagct tcatgaggag ttacttagct 780
ttgctctcct gtggacaggg catgcctgtg cctcccccaa gcacgggaaa aattggcata 840
gatgggccct tctcaaaaat cccactcctg gagcactggc caaaattact accatcctga 900
tgctgggctt gcagtccttt cctttgggaa tatgaacatg gtcaaaatta agtgaacgtg 960
tctttctggc tttctgtaca atggagcaga acaaagtatc aatttaacta aaatttgaac 1020
taaatectct ttccaggttt gga atg cac ttc tgt gga ggc acc ttg ata tcc 1073

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Met His Phe Cys Gly Gly Thr Leu Ile Ser

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          1           5           10
cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc cca agg 1121
Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg
          15           20           25
cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc 1169
Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu
          30           35           40
gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg gag ccc 1217
Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro
          45           50           55
aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc gtc atc 1265
Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val Ile
          60           65           70
act gac aaa gta atc cca gct tgt ctg cca tcc cca aat tat gtg gtc 1313
Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Pro Asn Tyr Val Val
          75           80           85           90
gct gac cgg acc gaa tgt ttc atc act ggc tgg gga gaa acc caa ggt 1361
Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly
          95           100          105
act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc cct gtg att gag 1409
Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val Ile Glu
          110          115          120
aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc caa tcc 1457
Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser
          125          130          135
acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag 1505
Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln
          140          145          150
ggg gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa tac att 1553
Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile
          155          160          165          170

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tta caa gga gtc act tct tgg ggt ctt ggc tgt gca cgc ccc aat aag 1601
Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys
      175      180      185
cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act tgg att gag gga 1649
Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly
      190      195      200
gtg atg aga aat aat taattggacg ggagacagag tgacgcactg actcacctag 1704
Val Met Arg Asn Asn
      205
aggctggaac gtgggtaggg atttagcatg ctggaaataa ctggcagtaa tcaaacgaag 1764
acactgtccc cagctaccag ctatgccaaa cctcggcatt ttttgtgtta ttttctgact 1824
gctggattct gtagtaagggt gacatagcta tgacatttgt taaaaataaa ctctgtactt 1884
aactttgaaa aaaaaaaaaa aaa 1907

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<210> 54  
 <211> 207  
 <212> PRT  
 <213> Homo sapiens

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<400> 54
Met His Phe Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr
1      5      10      15
Ala Ala His Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val
      20      25      30
Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
      35      40      45
Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
      50      55      60
Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
65      70      75      80
Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
      85      90      95
Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
      100     105     110
Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg
      115     120     125
Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
      130     135     140
His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
145     150     155     160
Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
      165     170     175
Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
      180     185     190
Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
      195     200     205

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<210> 55  
 <211> 809  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..25





Lys Ser Pro Asp Phe Met Asn Ser Phe Arg Ile His Phe Trp Gly Cys  
 190 195 200  
 tgatgtagcg gcaaatacct gacatggcag cctcgaggga gaccacagga atcgaacccc 688  
 ctccagcact ggaggagct ggtttgaagt atgactttgt actgggcca cactcacctc 748  
 tagaatattg tttattagat aaaagaaaaa gcttttcctt agcccgaata aaaaaaaaaa 808  
 t 809

<210> 56  
 <211> 201  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Leu Glu Val Ser Asp Ala Leu Gly Gly Pro Gly Arg Val Pro Gly  
 1 5 10 15  
 Ala Thr Ala Gly Met Asn Gly Val Asp Thr Ser Leu Leu Cys Asp Leu  
 20 25 30  
 Leu Gln Ala Leu Thr Phe Leu Thr Arg Asn Glu Ile Leu Cys Ile His  
 35 40 45  
 Asp Thr Phe Leu Lys Leu Cys Pro Pro Gly Lys Tyr Lys Glu Ala  
 50 55 60  
 Thr Leu Thr Met Asp Gln Val Ser Ser Leu Pro Ala Leu Arg Val Asn  
 65 70 75 80  
 Pro Phe Arg Asp Arg Ile Cys Arg Val Phe Ser His Lys Gly Met Phe  
 85 90 95  
 Ser Phe Glu Asp Val Leu Gly Met Ala Ser Val Phe Ser Glu Gln Ala  
 100 105 110  
 Cys Pro Ser Leu Lys Ile Glu Tyr Ala Phe Arg Ile Tyr Asp Phe Asn  
 115 120 125  
 Glu Asn Gly Phe Ile Asp Glu Glu Asp Leu Gln Arg Ile Ile Leu Arg  
 130 135 140  
 Leu Leu Asn Ser Asp Asp Met Ser Glu Asp Leu Leu Met Asp Leu Thr  
 145 150 155 160  
 Asn His Val Leu Ser Glu Ser Asp Leu Asp Asn Asp Asn Met Leu Ser  
 165 170 175  
 Phe Ser Glu Phe Glu His Ala Met Ala Lys Ser Pro Asp Phe Met Asn  
 180 185 190  
 Ser Phe Arg Ile His Phe Trp Gly Cys  
 195 200

<210> 57  
 <211> 1133  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..475

<220>  
 <221> CDS  
 <222> 476..964

<220>  
 <221> 3'UTR

<222> 965..1133

<220>

<221> polyA\_signal

<222> 1101..1106

<220>

<221> polyA\_site

<222> 1118..1133

<400> 57

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gagccaggag gtggcaggac gagttaggag gctggttcag tagctcgggc aagagcaggg   120
ccccccagga tctgaaggcc tcccaggccc cccaggccca gcgggtccca gaggagagcg   180
aggaccccaa ggtaactccg gtgagaaggc cgaccaggga tttcaaggcc agccaggctt   240
tccgggcccc ccgggtcccc ctggattccc aggcaaagtt ggatcacctg gccacactgg   300
ccctcaagca gagaaggcca gcgaagggat tcgaggccca tcaggcctgc ctgggtcccc   360
tgggccaccg ggacctctg ggattcaggg cccgcgcggg ctggatgggt tggatgggaa   420
ggatggcaag cctggcttga ggggggaccc tggctctgct ggccccctg gactc atg   478
                                     Met
                                     1
gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga   526
Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
                    5                      10                      15
cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg   574
Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
                    20                      25                      30
cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc   622
Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
                    35                      40                      45
ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga   670
Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
                    50                      55                      60                      65
cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc   718
Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
                    70                      75                      80
gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt   766
Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
                    85                      90                      95
cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg   814
Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
                    100                     105                     110
ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc   862
Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met Gly
                    115                     120                     125
cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc   910
Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
                    130                     135                     140                     145
atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct   958
Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro
                    150                     155                     160
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg   1014
Phe Gly
ccaaagctta taggactctg tgacagggtt tgaatgtttt tttgttggtt gttgttggtt 1074
ttaattgctg ttaatatattt ttaaataata aagaaacaaa actaaaaaaaa aaaaaaaaaa 1133

```

<210> 58  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Met Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro  
 1 5 10 15  
 Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly  
 20 25 30  
 Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg  
 35 40 45  
 Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro  
 50 55 60  
 Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala  
 65 70 75 80  
 Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro  
 85 90 95  
 Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro  
 100 105 110  
 Met Gly Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met  
 115 120 125  
 Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly  
 130 135 140  
 Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly  
 145 150 155 160  
 Pro Phe Gly

<210> 59  
 <211> 838  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..78

<220>  
 <221> CDS  
 <222> 79..642

<220>  
 <221> 3'UTR  
 <222> 643..838

<220>  
 <221> polyA\_signal  
 <222> 799..804

<220>  
 <221> polyA\_site  
 <222> 823..838

<400> 59

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aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggtctc 60
cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
1 5 10
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
15 20 25
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
30 35 40
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
45 50 55
gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
60 65 70 75
gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
80 85 90
gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
95 100 105
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
110 115 120
cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
125 130 135
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
140 145 150 155
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
160 165 170
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
175 180 185
aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccacct 692
Lys
gaccctccc tcagctgtcc tgtgccccgc cctctcccg cactcagtc cccctgctg 752
gcgttctctgc cgcagctctg acctggtgct gtgcacctgg catcttaata aamcctgctt 812
atacttcctt aaaaaaaaaa aaaaaa 838

```

<210> 60  
 <211> 188  
 <212> PRT  
 <213> Homo sapiens

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<400> 60
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1 5 10 15
Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
20 25 30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
35 40 45

```

```

Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
  50          55          60
Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
  65          70          75          80
Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala
          85          90          95
Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe
          100          105          110
Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala
          115          120          125
Trp Val Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu
          130          135          140
Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met
          145          150          155          160
Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu
          165          170          175
Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
          180          185

```

```

<210> 61
<211> 862
<212> DNA
<213> Homo sapiens

```

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<220>
<221> 5'UTR
<222> 1..158

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<220>
<221> CDS
<222> 159..764

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<220>
<221> 3'UTR
<222> 765..862

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<400> 61
attttttttt ttggcacgcc tgcagccaag ttggggaggg tttcctggac agaggtcctt 60
tggtctgctgc ctttaagacgt gcagcctggg ccgtggctgt cactgcgttc ggaccagac 120
ccgctgcagg cagcagcagc ccccgcccgc gcagcagc atg gag ctc tgg ggg gcc 176
                                Met Glu Leu Trp Gly Ala
                                -20          -15
tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu
          -10          -5          1
cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
          5          10          15
gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
          20          25          30
gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
          35          40          45          50
tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416

```

```

Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
      55      60      65
cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464
Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
      70      75      80
ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512
Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
      85      90      95
gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560
Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly
      100      105      110
ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
      115      120      125      130
cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
      135      140      145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
      150      155      160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
      165      170      175
ttc ggg atc gtg tagccggcgg ggcggggggcc gtggggggggc tggaggaggg 804
Phe Gly Ile Val
      180
caggagccgc gggaggccgg gaggagggtg gggaccttgc agccccatc ctctccgt 862

```

<210> 62  
 <211> 202  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..21

```

<400> 62
Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
      -20      -15      -10
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
      -5      1      5      10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
      15      20      25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
      30      35      40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
      45      50      55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
      60      65      70      75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
      80      85      90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
      95      100      105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp

```

110	115	120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu		
125	130	135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu		
140	145	150
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln		
160	165	170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val		
175	180	

<210> 63  
 <211> 618  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..194

<220>  
 <221> CDS  
 <222> 195..587

<220>  
 <221> 3'UTR  
 <222> 588..618

<220>  
 <221> polyA\_signal  
 <222> 578..583

<220>  
 <221> polyA\_site  
 <222> 604..618

<400> 63  
 atttgcttag gtctgatcaa tctgctccac acaattttctc agtgatcctc tgcattctctg 60  
 cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120  
 ttctgttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180  
 acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230  
                   Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu  
                   -20                  -15                  -10  
 act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278  
 Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala  
                   -5                  1                  5  
 cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326  
 Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln  
                   10                  15                  20  
 agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374  
 Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala  
                   25                  30                  35  
 tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422  
 Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr  
                   40                  45                  50                  55  
 aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470



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Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
      60      65      70
atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
      75      80      85
act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctc atg 566
Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
      90      95     100
tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
Cys Phe Ala Leu Leu Asn Cys
      105     110

```

<210> 64  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..22

```

<400> 64
Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
      -20      -15      -10
Leu Ala Ile Leu Ala Ile Leu Thr Arg Trp Ala Arg Arg Lys Gln
      -5      1      5      10
Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
      15      20      25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
      30      35      40
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
      45      50      55
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
      60      65      70
Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg Thr Ala Gly Ala
      75      80      85      90
Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met Cys Phe Ala Leu
      95     100     105
Leu Asn Cys

```

<210> 65  
 <211> 836  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..176

<220>  
 <221> CDS  
 <222> 177..767

<220>  
 <221> 3'UTR

<222> 768..836

<220>

<221> polyA\_signal

<222> 814..819

<220>

<221> polyA\_site

<222> 822..836

<400> 65

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aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgcctacaag ggccctccctg 60
acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120
ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaataca tggaaa atg 179
Met
aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
-20 -15 -10 -5
gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
1 5 10
gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
15 20 25
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
30 35 40
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg 419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
45 50 55 60
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa 467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
65 70 75
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg 515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
80 85 90
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
95 100 105
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct 611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
110 115 120
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc 659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
125 130 135 140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc 707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
145 150 155
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt 755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
160 165 170
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg 807
Phe Ser Pro Ala
175
atagtgata aatgaaaaaa aaaaaaaaaa 836

```

<210> 66  
 <211> 197  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..22

<400> 66  
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly  
           -20                  -15                  -10  
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln  
       -5                          1                  5                  10  
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu  
                   15                          20                  25  
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln  
                   30                          35                  40  
 Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala  
           45                          50                  55  
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile  
       60                          65                  70  
 Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala  
 75                          80                          85                  90  
 Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys  
                   95                          100                  105  
 Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr  
                   110                          115                  120  
 Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp  
           125                          130                  135  
 Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn  
       140                          145                  150  
 Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser  
 155                          160                          165                  170  
 Leu Phe Ser Pro Ala  
                           175

<210> 67  
 <211> 789  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..62

<220>  
 <221> CDS  
 <222> 63..572

<220>  
 <221> 3'UTR  
 <222> 573..789

<220>  
 <221> polyA\_signal  
 <222> 750..755

<220>  
 <221> polyA\_site  
 <222> 774..789

<400> 67  
 atatgtcatc agggcccccg cctgggaggt gtgctgccag agattttgcc ttttcaaggt 60  
 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107  
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly  
 1 5 10 15  
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155  
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys  
 20 25 30  
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203  
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu  
 35 40 45  
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251  
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu  
 50 55 60  
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299  
 Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro  
 65 70 75  
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347  
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val  
 80 85 90 95  
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395  
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu  
 100 105 110  
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443  
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile  
 115 120 125  
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491  
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr  
 130 135 140  
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539  
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro  
 145 150 155  
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592  
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp  
 160 165 170  
 gaggagggac gccagggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652  
 caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712  
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772  
 gaaaaaaaaa aaaaaaa 789

<210> 68  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro

```

1           5           10           15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
                20           25           30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
                35           40           45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
                50           55           60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65           70           75           80
Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
                85           90           95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
                100          105          110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
                115          120          125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
                130          135          140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145          150          155          160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
                165          170

```

<210> 69  
 <211> 2556  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..66

<220>  
 <221> CDS  
 <222> 67..2427

<220>  
 <221> 3'UTR  
 <222> 2428..2556

<220>  
 <221> polyA\_signal  
 <222> 2522..2527

<220>  
 <221> polyA\_site  
 <222> 2541..2556

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<400> 69
gtccccgcgt ccctggcaat tcccgaattc ccaacggctt cctgctggca gccccgaagc 60
cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108
      Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu
      -15           -10           -5
ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
      1           5           10           15

```

cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat	204
Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr	
20 25 30	
gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg	252
Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val	
35 40 45	
cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg	300
His Leu Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu	
50 55 60	
tac aat caa gga tct atg aat act tat tct tca gat att cag act caa	348
Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln	
65 70 75	
tgc tac tat caa gga aat att gaa gaa tat cca gat tcc atg gtc aca	396
Cys Tyr Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr	
80 85 90 95	
ctc agc acg tgc tct gga cta aga gga ata ctg caa ttt gaa aat gtt	444
Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val	
100 105 110	
tct tat gga att gag cct ctg gaa tct gca gtt gaa ttt cag cat gtt	492
Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val	
115 120 125	
ctt cac aaa tta aag aat gaa gac aat gat att gca att ttt att gac	540
Leu His Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp	
130 135 140	
aga agc ctg aaa gaa caa cca atg gat gac aac att ttt ata agt gaa	588
Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu	
145 150 155	
aaa tca gaa cca gct gtt cca gat tta ttt cct ctt tat cta gaa atg	636
Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met	
160 165 170 175	
cat att gtg gtg gac aaa act ttg tat gat tac tgg ggc tct gat agc	684
His Ile Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser	
180 185 190	
atg ata gta aca aat aaa gtc atc gaa att gtt ggc ctt gca aat tca	732
Met Ile Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser	
195 200 205	
atg ttc acc caa ttt aaa gtt act att gtg ctg tca tca ttg gag tta	780
Met Phe Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu	
210 215 220	
tgg tca gat gaa aat aag att tct aca gtt ggt gag gca gat gaa tta	828
Trp Ser Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu	
225 230 235	
ttg caa aaa ttt tta gaa tgg aaa caa tct tat ctt aac cta agg cct	876
Leu Gln Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro	
240 245 250 255	
cat gat att gca tat cta cta att tat atg gat tat cct cgt tat ttg	924
His Asp Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu	
260 265 270	
gga gca gtg ttt cct gga aca atg tgt att act cgt tat tct gca gga	972
Gly Ala Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly	
275 280 285	
gtc gca ttg tac ccc aag gag ata act ctg gag gca ttt gca gtt att	1020
Val Ala Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile	
290 295 300	
gtc acc cag atg ctg gca ctc agt ctg gga ata tca tat gac gac cca	1068

Val	Thr	Gln	Met	Leu	Ala	Leu	Ser	Leu	Gly	Ile	Ser	Tyr	Asp	Asp	Pro	
305						310					315					
aag	aaa	tgt	caa	tgt	tca	gaa	tcc	acc	tgt	ata	atg	aat	cca	gaa	gtt	1116
Lys	Lys	Cys	Gln	Cys	Ser	Glu	Ser	Thr	Cys	Ile	Met	Asn	Pro	Glu	Val	
320						325					330				335	
gtg	caa	tcc	aat	ggg	gtg	aag	act	ttt	agc	agt	tgc	agt	ttg	agg	agc	1164
Val	Gln	Ser	Asn	Gly	Val	Lys	Thr	Phe	Ser	Ser	Cys	Ser	Leu	Arg	Ser	
				340						345					350	
ttt	caa	aat	ttc	att	tca	aat	gtg	ggg	gtc	aaa	tgt	ctt	cag	aat	aag	1212
Phe	Gln	Asn	Phe	Ile	Ser	Asn	Val	Gly	Val	Lys	Cys	Leu	Gln	Asn	Lys	
				355					360					365		
cca	caa	atg	caa	aaa	aaa	tct	ccg	aaa	cca	gtc	tgt	ggc	aat	ggc	aga	1260
Pro	Gln	Met	Gln	Lys	Lys	Ser	Pro	Lys	Pro	Val	Cys	Gly	Asn	Gly	Arg	
				370				375				380				
ttg	gag	gga	aat	gaa	atc	tgt	gat	tgt	ggg	act	gag	gct	caa	tgt	gga	1308
Leu	Glu	Gly	Asn	Glu	Ile	Cys	Asp	Cys	Gly	Thr	Glu	Ala	Gln	Cys	Gly	
				385			390				395					
cct	gca	agc	tgt	tgt	gat	ttt	cga	act	tgt	gta	ctg	aaa	gac	gga	gca	1356
Pro	Ala	Ser	Cys	Cys	Asp	Phe	Arg	Thr	Cys	Val	Leu	Lys	Asp	Gly	Ala	
400					405					410					415	
aaa	tgt	tat	aaa	gga	ctg	tgc	tgc	aaa	gac	tgt	caa	att	tta	caa	tca	1404
Lys	Cys	Tyr	Lys	Gly	Leu	Cys	Cys	Lys	Asp	Cys	Gln	Ile	Leu	Gln	Ser	
				420					425						430	
ggc	gtt	gaa	tgt	agg	ccg	aaa	gca	cat	cct	gaa	tgt	gac	atc	gct	gaa	1452
Gly	Val	Glu	Cys	Arg	Pro	Lys	Ala	His	Pro	Glu	Cys	Asp	Ile	Ala	Glu	
				435				440						445		
aat	tgt	aat	gga	agc	tca	cca	gaa	tgt	ggg	cct	gac	ata	act	tta	atc	1500
Asn	Cys	Asn	Gly	Ser	Ser	Pro	Glu	Cys	Gly	Pro	Asp	Ile	Thr	Leu	Ile	
				450				455						460		
aat	gga	ctt	tca	tgc	aaa	aat	aat	aag	ttt	att	tgt	tat	gac	gga	gac	1548
Asn	Gly	Leu	Ser	Cys	Lys	Asn	Asn	Lys	Phe	Ile	Cys	Tyr	Asp	Gly	Asp	
				465				470			475					
tgc	cat	gat	ctc	gat	gca	cgt	tgt	gag	agt	gta	ttt	gga	aaa	ggg	tca	1596
Cys	His	Asp	Leu	Asp	Ala	Arg	Cys	Glu	Ser	Val	Phe	Gly	Lys	Gly	Ser	
480					485					490					495	
aga	aat	gct	cca	ttt	gcc	tgc	tat	gaa	gaa	ata	caa	tct	caa	tca	gac	1644
Arg	Asn	Ala	Pro	Phe	Ala	Cys	Tyr	Glu	Glu	Ile	Gln	Ser	Gln	Ser	Asp	
				500						505					510	
aga	ttt	ggg	aac	tgt	ggg	agg	gat	aga	aat	aac	aaa	tat	gtg	ttc	tgt	1692
Arg	Phe	Gly	Asn	Cys	Gly	Arg	Asp	Arg	Asn	Asn	Lys	Tyr	Val	Phe	Cys	
				515				520						525		
gga	tgg	agg	aat	ctt	ata	tgt	gga	aga	tta	gtt	tgt	acc	tac	cct	act	1740
Gly	Trp	Arg	Asn	Leu	Ile	Cys	Gly	Arg	Leu	Val	Cys	Thr	Tyr	Pro	Thr	
				530				535						540		
cga	aag	cct	ttc	cat	caa	gaa	aat	ggg	gat	gtg	att	tat	gct	ttc	gta	1788
Arg	Lys	Pro	Phe	His	Gln	Glu	Asn	Gly	Asp	Val	Ile	Tyr	Ala	Phe	Val	
				545				550							555	
cga	gat	tct	gta	tgc	ata	acc	gta	gac	tac	aaa	ttg	cct	cga	aca	gtt	1836
Arg	Asp	Ser	Val	Cys	Ile	Thr	Val	Asp	Tyr	Lys	Leu	Pro	Arg	Thr	Val	
560					565					570					575	
cca	gat	cca	ctg	gct	gtc	aaa	aat	ggc	tct	cag	tgt	gat	att	ggg	agg	1884
Pro	Asp	Pro	Leu	Ala	Val	Lys	Asn	Gly	Ser	Gln	Cys	Asp	Ile	Gly	Arg	
				580					585					590		
gtt	tgt	gta	aat	cgt	gaa	tgt	gta	gaa	tca	agg	ata	att	aag	gct	tca	1932
Val	Cys	Val	Asn	Arg	Glu	Cys	Val	Glu	Ser	Arg	Ile	Ile	Lys	Ala	Ser	

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      595      600      605
gca cat gtt tgt tca caa cag tgt tct gga cat gga gtg tgt gat tcc 1980
Ala His Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser
      610      615      620
aga aac aag tgc cat tgt tcg cca ggc tat aag cct cca aac tgc caa 2028
Arg Asn Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln
      625      630      635
ata cgt tcc aaa gga ttt tcc ata ttt cct gag gaa gat atg ggt tca 2076
Ile Arg Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser
      640      645      650      655
atc atg gaa aga gca tct ggg aag act gaa aac acc tgg ctt cta ggt 2124
Ile Met Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly
      660      665      670
ttc ctc att gct ctt cct att ctc att gta aca acc gca ata gtt ttg 2172
Phe Leu Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu
      675      680      685
gca agg aaa cag ttg aaa aac tgg ttc gcc aag gaa gag gaa ttc cca 2220
Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro
      690      695      700
agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa 2268
Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln
      705      710      715
tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca 2316
Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
      720      725      730      735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
      740      745      750
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
      755      760      765
caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
Gln Ser Ser Ser Asn
      770
tcgctaagaa atgaaaattc tgtctttcct tccgtgggtca cagctgaaag aaacaataaa 2527
ttgagtgtgg accaaaaaaa aaaaaaaat 2556

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<210> 70  
 <211> 787  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..16

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<400> 70
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  -15      -10      -5
Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
  1      5      10      15
Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
      20      25      30
Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
      35      40      45

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Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn  
 50 55 60  
 Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr  
 65 70 75 80  
 Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser  
 85 90 95  
 Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr  
 100 105 110  
 Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His  
 115 120 125  
 Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser  
 130 135 140  
 Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser  
 145 150 155 160  
 Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile  
 165 170 175  
 Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile  
 180 185 190  
 Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe  
 195 200 205  
 Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser  
 210 215 220  
 Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln  
 225 230 235 240  
 Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp  
 245 250 255  
 Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala  
 260 265 270  
 Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala  
 275 280 285  
 Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr  
 290 295 300  
 Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys  
 305 310 315 320  
 Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln  
 325 330 335  
 Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln  
 340 345 350  
 Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln  
 355 360 365  
 Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu  
 370 375 380  
 Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala  
 385 390 395 400  
 Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys  
 405 410 415  
 Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val  
 420 425 430  
 Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys  
 435 440 445  
 Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly  
 450 455 460  
 Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His  
 465 470 475 480  
 Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn

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      485      490      495
Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe
      500      505      510
Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp
      515      520      525
Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys
      530      535      540
Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp
545      550      555      560
Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp
      565      570      575
Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys
      580      585      590
Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His
      595      600      605
Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn
      610      615      620
Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg
625      630      635      640
Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met
      645      650      655
Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu
      660      665      670
Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg
      675      680      685
Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser
      690      695      700
Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser
705      710      715      720
Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser
      725      730      735
Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu
      740      745      750
Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser
      755      760      765
Ser Ser Asn
      770

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<210> 71
<211> 1603
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..7

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<220>
<221> CDS
<222> 8..763

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<220>
<221> 3'UTR
<222> 764..1603

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<220>  
 <221> polyA\_signal  
 <222> 1562..1567

<220>  
 <221> polyA\_site  
 <222> 1588..1603

<220>  
 <221> MISC\_FEATURE  
 <222> 157  
 <223> Xaa = Ala,Gly

<400> 71  
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                   -15                                  -10                                  -5  
 cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca 97  
 Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro  
           1                                  5                                  10  
 cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc 145  
 His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu  
 15                                  20                                  25                                  30  
 ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata 193  
 Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile  
                                   35                                  40                                  45  
 gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt 241  
 Ala Ala Thr Pro Ala Ser Ala Ala Ala Ala Thr Leu Asp Val Ala Val  
                   50                                  55                                  60  
 cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg 289  
 Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu  
           65                                  70                                  75  
 gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg 337  
 Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu  
           80                                  85                                  90  
 tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat 385  
 Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His  
 95                                  100                                  105                                  110  
 gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc 433  
 Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile  
                   115                                  120                                  125  
 ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg 481  
 Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val  
                   130                                  135                                  140  
 ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca 529  
 Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala  
           145                                  150                                  155  
 ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc 577  
 Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala  
           160                                  165                                  170  
 ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg 625  
 Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg  
 175                                  180                                  185                                  190  
 gtg ctg aat gga gag gca cct cct agc cta ggc cct tcc tct gtg gcc 673  
 Val Leu Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala

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                195                200                205
tcc cca gag gac gtc cag gcc ctg atg tac ctg aga ggg cag ctg gag   721
Ser Pro Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu
                210                215                220
cct cag tgg aag atg ttg cag tgc cat cct cac ctg gtg gct           763
Pro Gln Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
                225                230                235
tgaaatcggc caaggtggga gcattttacac cgcagaaatg acaccgcacg ccagcgcccc   823
gcgggccgca tccggacccc aagcccacgg ctccctcgac tctggggcac ggaaccccgc   883
ccactcccaa tccccgcgcc ccgccctctc ccaccctgtc ttcccccgct ccaccctca   943
cctcacctcg cccccgcccc acccatcgcg ccccgggcggc tggtattgtt cggctgggct 1003
cggtcggggc ctgtctccct cggtctcgcg ggtgtcagtt cgtccggctt cctcacagcc 1063
cctcactccc ggcggtctgac agcagcagcg gcggcgggcg gcggcgctg gcgtttcgag 1123
gctgagcggc accgggggtg gggcgcgagg gaggagcagc agcgggagga ggagccgtgt 1183
gccctggcac tgagcggccg cggccatggc gtacgcctat ctcttcaagt acatcataat 1243
cggcgacaca ggtgttggtg aatcatgctt attgctacag tttacagaca agaggttcag 1303
ccagtgcatt accttactat tgggtgtagag ttcggtgctc gaatgataac tattgatggg 1363
aaacagataa aacttcagat atgggatacg gcagggcaag aatcctttcg ttccatcaca 1423
aggtcgtatt acagaggtgc agcaggagct ttactagttt acgatattac acggagagat 1483
acattcaacc acttgacaac ctggttagaa gatgcccgcc agcattccaa ttccaacatg 1543
gtcattatgc ttattggaaa taaaagtgat ttagaatcta gaagaaaaaa aaaaagaaaa 1603

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<210> 72

<211> 252

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..17

<220>

<221> MISC\_FEATURE

<222> 156

<223> Xaa = Ala,Gly

<400> 72

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Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro His Glu
      1                5                10                15
Ser Leu Ala Arg Glu Ala Leu Thr Ala Leu Gly Lys Leu Leu Tyr
      20                25                30
Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile Ala Ala
      35                40                45
Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val Arg Arg
      50                55                60
Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu Gly Gln
      65                70                75
Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu Trp Leu
      80                85                90                95
Asn Ile Arg Gly Lys Glu Ala Ala Ala Leu Ser Met Phe His Val Ser
      100               105               110
Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile Leu Gly
      115               120               125

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Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val Leu Val
      130      135      140
Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala Leu Leu
      145      150      155
Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala Leu Leu
160      165      170      175
Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg Val Leu
      180      185      190
Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala Ser Pro
      195      200      205
Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu Pro Gln
      210      215      220
Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
      225      230      235

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<210> 73
<211> 879
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..8

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<220>
<221> CDS
<222> 9..395

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<220>
<221> 3'UTR
<222> 396..879

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<220>
<221> polyA_site
<222> 864..879

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      Met Ala Val Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly
      -15      -10      -5
cca ggc ccg ggt cct cgg ccg ctg tgg ggc cca ggc ccg gcc tgg agt 98
Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser
      1      5      10      15
cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146
Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
      20      25      30
agg cct ccg ggg gac ctc gcc gag gct gga ggc cga gct ctg cag agc 194
Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
      35      40      45
tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242
Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu
      50      55      60
ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt 290
Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu
      65      70      75

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tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat 338
Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn
80      85      90      95
aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt 386
Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly
100      105      110
ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac 435
Ile Phe Ile
rtttctgttt wccttttagc aaggtgaaac cagtctggam aatggggaga tgggcccgggt 495
gcagtggctc acacttgtaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga 555
ggcctatacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtggtggc 615
tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacct gcaccctggc 675
caacatggtg aaaccccgtc ttactaaaa atagaaaatt agccgggcgt gatggcacac 735
gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggaggtg 795
gaggttgctg tgagtggaga tcatgccatt gactccagc ctgagcaaca agagcaaaac 855
tccatcccaa aaaaaaaaaa aaaa 879

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<210> 74
<211> 129
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> 1..16

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<400> 74
Met Ala Val Leu Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly Pro Gly
-15      -10      -5
Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
1      5      10      15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
20      25      30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
35      40      45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
50      55      60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
65      70      75      80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
85      90      95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
100      105      110
Ile

```

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<210> 75
<211> 1634
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..87

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<220>

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<221> CDS  
 <222> 88..1269

<220>  
 <221> 3'UTR  
 <222> 1270..1634

<220>  
 <221> polyA\_signal  
 <222> 1594..1599

<220>  
 <221> polyA\_site  
 <222> 1619..1634

<400> 75  
 aaagttcctc agcccttggc tcctgcccag tgtttagggg gttggcggag acaaagggga 60  
 agagtcatcg cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114  
 Met Met Gly Val Phe Val Val Ala Ala  
 1 5  
 aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162  
 Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr  
 10 15 20 25  
 gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210  
 Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly  
 30 35 40  
 aaa gtc tca cct gaa aca gtt gac agt gtg att atg ggc aat gtc ctg 258  
 Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu  
 45 50 55  
 cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306  
 Gln Ser Ser Ser Asp Ala Ile Tyr Leu Ala Arg His Val Gly Leu Arg  
 60 65 70  
 gtg gga atc cca aag gag acc cca gct ctc acg att aat agg ctc tgt 354  
 Val Gly Ile Pro Lys Glu Thr Pro Ala Leu Thr Ile Asn Arg Leu Cys  
 75 80 85  
 ggt tct ggt ttt cag tcc att gtg aat gga tgt cag gaa att tgt gtt 402  
 Gly Ser Gly Phe Gln Ser Ile Val Asn Gly Cys Gln Glu Ile Cys Val  
 90 95 100 105  
 aaa gaa gct gaa gtt gtt tta tgt gga gga acc gaa agc atg agc caa 450  
 Lys Glu Ala Glu Val Leu Cys Gly Gly Thr Glu Ser Met Ser Gln  
 110 115 120  
 gct ccc tac tgt gtc aga aat gtg cgt ttt gga acc aag ctt gga tca 498  
 Ala Pro Tyr Cys Val Arg Asn Val Arg Phe Gly Thr Lys Leu Gly Ser  
 125 130 135  
 gat atc aag ctg gaa gat tct tta tgg gta tca tta aca gat cag cat 546  
 Asp Ile Lys Leu Glu Asp Ser Leu Trp Val Ser Leu Thr Asp Gln His  
 140 145 150  
 gtc cag ctc ccc atg gca atg act gca gag aat ctt gct gta aaa cac 594  
 Val Gln Leu Pro Met Ala Met Thr Ala Glu Asn Leu Ala Val Lys His  
 155 160 165  
 aaa ata agc aga gaa gaa tgt gac aaa tat gcc ctg cag tca cag cag 642  
 Lys Ile Ser Arg Glu Glu Cys Asp Lys Tyr Ala Leu Gln Ser Gln Gln  
 170 175 180 185  
 aga tgg aaa gct gct aat gat gct ggc tac ttt aat gat gaa atg gca 690  
 Arg Trp Lys Ala Ala Asn Asp Ala Gly Tyr Phe Asn Asp Glu Met Ala

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      190      195      200
cca att gaa gtg aag aca aag aaa gga aaa cag aca atg cag gta gac 738
Pro Ile Glu Val Lys Thr Lys Lys Gly Lys Gln Thr Met Gln Val Asp
      205      210      215
gag cat gct cgg ccc caa acc acc ctg gaa cag tta cag aaa ctt cct 786
Glu His Ala Arg Pro Gln Thr Thr Leu Glu Gln Leu Gln Lys Leu Pro
      220      225      230
cca gta ttc aag aaa gat gga act gtt act gca ggg aat gca tcg ggt 834
Pro Val Phe Lys Lys Asp Gly Thr Val Thr Ala Gly Asn Ala Ser Gly
      235      240      245
gta gct gat ggt gct gga gct gtt atc ata gct agt gaa gat gct gtt 882
Val Ala Asp Gly Ala Gly Ala Val Ile Ile Ala Ser Glu Asp Ala Val
      250      255      260      265
aag aaa cat aac ttc aca cca ctg gca aga att gtg ggc tac ttt gta 930
Lys Lys His Asn Phe Thr Pro Leu Ala Arg Ile Val Gly Tyr Phe Val
      270      275      280
tct gga tgt gat ccc tct atc atg ggt att ggt cct gtc cct gct atc 978
Ser Gly Cys Asp Pro Ser Ile Met Gly Ile Gly Pro Val Pro Ala Ile
      285      290      295
agt ggg gca ctg aag aaa gca gga ctg agt ctt aag gac atg gat ttg 1026
Ser Gly Ala Leu Lys Lys Ala Gly Leu Ser Leu Lys Asp Met Asp Leu
      300      305      310
gta gag gtg aat gaa gct ttt gct ccc cag tac ttg gct gtt gag agg 1074
Val Glu Val Asn Glu Ala Phe Ala Pro Gln Tyr Leu Ala Val Glu Arg
      315      320      325
agt ttg gat ctt gac ata agt aaa acc aat gtg aat gga gga gcc att 1122
Ser Leu Asp Leu Asp Ile Ser Lys Thr Asn Val Asn Gly Gly Ala Ile
      330      335      340      345
gct ttg ggt cac cca ctg gga gga tct gga tca aga att act gca cac 1170
Ala Leu Gly His Pro Leu Gly Gly Ser Gly Ser Arg Ile Thr Ala His
      350      355      360
ctg gtt cac gaa tta agg cgt cga ggt gga aaa tat gcc gtt gga tca 1218
Leu Val His Glu Leu Arg Arg Arg Gly Gly Lys Tyr Ala Val Gly Ser
      365      370      375
gct tgc att gga ggt ggc caa ggt att gct gtc atc att cag agc aca 1266
Ala Cys Ile Gly Gly Gly Gln Gly Ile Ala Val Ile Ile Gln Ser Thr
      380      385      390
gcc tgaagagacc agtgagctca ctgtgaccca tccttactct acttggccag 1319
Ala
gccacagtaa aacaagtgac cttcagagca gctgccacaa ctggccatgc cctgccattg 1379
aaacagtgat taagtttgat caagccatgg tgacacaaaa atgcattgat catgaatagg 1439
agcccatgct agaagtacat tctctcagat ttgaaccagt gaaatatgat gtatttctga 1499
gctaaaactc aactatagaa gacattaaaa gaaatcgtat tcttgccaag taaccaccac 1559
ttctgcctta gataatatga ttataaggaa atcaaataaa tgttgcctta acttcaaaca 1619
aaaaaaaaaa aaaaaa 1634

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<210> 76  
 <211> 394  
 <212> PRT  
 <213> Homo sapiens

<400> 76  
 Met Met Gly Val Phe Val Val Ala Ala Lys Arg Thr Pro Phe Gly Ala  
 1 5 10 15  
 Tyr Gly Gly Leu Leu Lys Asp Phe Thr Ala Thr Asp Leu Ser Glu Phe



20	25	30
Ala Ala Lys Ala Ala Leu Ser Ala Gly Lys Val Ser Pro Glu Thr Val		
35	40	45
Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Asp Ala Ile		
50	55	60
Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr		
65	70	75
Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile		
85	90	95
Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu		
100	105	110
Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn		
115	120	125
Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser		
130	135	140
Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met		
145	150	155
Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys		
165	170	175
Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp		
180	185	190
Ala Gly Tyr Phe Asn Asp Glu Met Ala Pro Ile Glu Val Lys Thr Lys		
195	200	205
Lys Gly Lys Gln Thr Met Gln Val Asp Glu His Ala Arg Pro Gln Thr		
210	215	220
Thr Leu Glu Gln Leu Gln Lys Leu Pro Pro Val Phe Lys Lys Asp Gly		
225	230	235
Thr Val Thr Ala Gly Asn Ala Ser Gly Val Ala Asp Gly Ala Gly Ala		
245	250	255
Val Ile Ile Ala Ser Glu Asp Ala Val Lys Lys His Asn Phe Thr Pro		
260	265	270
Leu Ala Arg Ile Val Gly Tyr Phe Val Ser Gly Cys Asp Pro Ser Ile		
275	280	285
Met Gly Ile Gly Pro Val Pro Ala Ile Ser Gly Ala Leu Lys Lys Ala		
290	295	300
Gly Leu Ser Leu Lys Asp Met Asp Leu Val Glu Val Asn Glu Ala Phe		
305	310	315
Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser		
325	330	335
Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly		
340	345	350
Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg		
355	360	365
Arg Gly Gly Lys Tyr Ala Val Gly Ser Ala Cys Ile Gly Gly Gly Gln		
370	375	380
Gly Ile Ala Val Ile Ile Gln Ser Thr Ala		
385	390	

<210> 77  
 <211> 1642  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR

<222> 1..68

<220>

<221> CDS

<222> 69..875

<220>

<221> 3'UTR

<222> 876..1642

<220>

<221> polyA\_signal

<222> 1599..1604

<220>

<221> polyA\_site

<222> 1627..1642

<400> 77

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attttatagc ggccgcgggc ggccggcggca gcggttgag gttgtaggac cggcgaggaa      60
taggaatc atg gcg gct gcg ctg ttc gtg ctg ctg gga ttc gcg ctg ctg      110
      Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu
      -20              -15              -10
ggc acc cac gga gcc tcc ggg gct gcc ggc aca gtc ttc act acc gta      158
Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val
      -5              1              5              10
gaa gac ctt ggc tcc aag ata ctc ctc acc tgc tcc ttg aat gac agc      206
Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser
      15              20              25
gcc aca gag gtc aca ggg cac cgc tgg ctg aag ggg ggc gtg gtg ctg      254
Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu
      30              35              40
aag gag gac gcg ctg ccc ggc cag aaa acg gag ttc aag gtg gac tcc      302
Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser
      45              50              55
gac gac cag tgg gga gag tac tcc tgc gtc ttc ctc ccc gag ccc atg      350
Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met
      60              65              70
ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg      398
Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
      75              80              85              90
aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc      446
Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
      95              100              105
aag tca gag tcc gtg cca cct gtc act gac tgg gcc tgg tac aag atc      494
Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile
      110              115              120
act gac tct gag gac aag gcc ctc atg aac ggc tcc gag agc agg ttc      542
Thr Asp Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe
      125              130              135
ttc gtg agt tcc tcg cag ggc ctg tca gag cta cac att gag aac ctg      590
Phe Val Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu
      140              145              150
aac atg gag gcc gac ccc ggc cag tac cgg tgc aac ggc acc agc tcc      638
Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser

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155          160          165          170
aag ggc tcc gac cag gcc atc atc acg ctc cgc gtg cgc agc cac ctg      686
Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu
          175          180          185
gcc gcc ctc tgg ccc ttc ctg ggc atc gtg gct gag gtg ctg gtg ctg      734
Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu
          190          195          200
gtc acc atc atc ttc atc tac gag aag cgc cgg aag ccc gag gac gtc      782
Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val
          205          210          215
ctg gat gat gac gac gcc ggc tct gca ccc ctg aag agc agc ggg cag      830
Leu Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln
          220          225          230
cac cag aat gac aaa ggc aag aac gtc cgc cag agg aac tct tcc      875
His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
235          240          245
tgaggcaggt ggccccagga cgctccctgc tccgcgtctg cgccgccgcc ggagtccact 935
cccagtgtt gcaagattcc aagttctcac ctcttaaaga aaacccaccc cgtagattcc 995
catcatacac ttccttcttt tttaaaaaag ttgggttttc tccattcagg attctgttcc 1055
ttaggatttt ttccttctga agtgtttcac gagagcccgg gagctgtctg cctgcggccc 1115
cgtctgtggc tttcagcctc tgggtctgag tcatggccgg gtgggcggca cagccttctc 1175
cactggccgg agtcagtgcc aggtccttgc cctttgtgga aagtcacagg tcacacgagg 1235
ggccccgtgt cctgcctgtc tgaagccaat gctgtctggt tgcgccattt ttgtgctttt 1295
atgtttaatt ttatgagggc cacgggtctg tgttcgactc agcctcaggg acgactctga 1355
cctcttgccc acagaggact cacttgccca caccgagggc gaccccgta cagcctcaag 1415
tcactcccaa gcccctcct tgtctgtgca tccgggggca gctctggagg gggtttgctg 1475
gggaactggc gccatcgccg ggactccaga accgcagaag cctccccagc tcacccttgg 1535
aggacggccg gctctctata gcaccagggc tcacgtggga acccccctcc caccaccgac 1595
cacaataaag atcgccccca cctccaccct caaaaaaaaa aaaaaaaa      1642

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<210> 78  
 <211> 269  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..21

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<400> 78
Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr
-20          -15          -10
His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
-5          1          5          10
Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
15          20          25
Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
30          35          40
Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
45          50          55
Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
60          65          70          75
Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
80          85          90
Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser

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          95              100              105
Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
      110              115              120
Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
      125              130              135
Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met
140              145              150              155
Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
      160              165              170
Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
      175              180              185
Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
      190              195              200
Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
      205              210              215
Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
220              225              230              235
Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
      240              245

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<210> 79  
 <211> 1466  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..343

<220>  
 <221> CDS  
 <222> 344..1144

<220>  
 <221> 3'UTR  
 <222> 1145..1466

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<400> 79
attgtgactt tgggccaggc tgggggaaat gacccgggag ggtcccatgc ggctacataa 60
aattggcagc cttagaacta gtgggaaggc ggggtgcgcga agtcgagggg cggagagagg 120
gggccggagg agctgctttc tgaatccaag ttcgtgggct ctctcagaag tcctcaggac 180
ggagcagagg tggccggcgg gcccggtcga ctgcgcctyt gctttctttc cataaccttt 240
tctttcggac tcgaatcacg gctgctgcga agggcttagt tccggacact aggggtgcöcg 300
aacgcgctga tgccccgagt gctcgcaggg cttcccgcta acc atg ctg ccg ccg 355
                                     Met Leu Pro Pro
ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg 403
Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu
-25              -20              -15              -10
gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca 451
Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro
      -5              1              5
gat tac ctg cgg cgc ggc tgg atg cgg ctg cta gcg gag ggc gag ggc 499
Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly
      10              15              20
tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg 547

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Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro Arg Gly Cys Leu
 25      30      35
gcg ggc agg gtg cgc gac gcg tgc ggc tgc tgc tgg gaa tgc gcc aac 595
Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp Glu Cys Ala Asn
40      45      50      55
ctc gag ggc cag ctc tgc gac ctg gac ccc agt gct cac ttc tac ggg 643
Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala His Phe Tyr Gly
      60      65      70
cac tgc ggc gag cag ctt gag tgc cgg ctg gac aca ggc ggc gac ctg 691
His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr Gly Gly Asp Leu
      75      80      85
agc cgc gga gag gtg ccg gaa cct ctg tgt gcc tgt cgt tcg cag agt 739
Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys Arg Ser Gln Ser
      90      95      100
ccg ctc tgc ggg tcc gac ggt cac acc tac tcc cag atc tgc cgc ctg 787
Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln Ile Cys Arg Leu
      105      110      115
cag gag gcg gcc cgc gct cgg ccc gat gcc aac ctc act gtg gca cac 835
Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu Thr Val Ala His
      120      125      130      135
ccg ggg ccc tgc gaa tcg ggg ccc cag atc gtg tca cat cca tat gac 883
Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser His Pro Tyr Asp
      140      145      150
act tgg aat gtg aca ggg cag gat gtg atc ttt ggc tgt gaa gtg ttt 931
Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly Cys Glu Val Phe
      155      160      165
gcc tac ccc atg gcc tcc atc gag tgg agg aag gat ggc ttg gac atc 979
Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp Gly Leu Asp Ile
      170      175      180
cag ctg cca ggg gat gac ccc cac atc tct gtg cag ttt agg ggt gga 1027
Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln Phe Arg Gly Gly
      185      190      195
ccc cag agg ttt gag gtg act ggc tgg ctg cag atc cag gct gtg cgt 1075
Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile Gln Ala Val Arg
      200      205      210      215
ccc agt gat gag ggc act tac cgc tgc ctt ggc cca atg ccc tgg gtc 1123
Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro Met Pro Trp Val
      220      225      230
aag tgg agg ccc ctg cta gct tgacagtgct cacacctgac cagctgaact 1174
Lys Trp Arg Pro Leu Leu Ala
      235
ctacaggcat cccccagctg cgatcactaa acctggttcc tgaggaggag gctgagagtg 1234
aagagaatga cgattactac taggtccaga gctctggccc atgggggtgg gtgagcggct 1294
atagtgttca tccctgctct tgaaaagacc tggaaagggg agcaggggtcc cttcatcgac 1354
tgctttcatg ctgtcagtag ggatgatcat gggaggccta tttgactcca aggtagcagt 1414
gtggtaggat agagacaaaa gctggaggag ggtagggaga gaagctgaga cc 1466

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<210> 80  
 <211> 267  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..30

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<400> 80
Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu
-30          -25          -20          -15
Leu Leu Leu Leu Val Val Leu Thr Pro Pro Thr Gly Ala Arg Pro
          -10          -5          1
Ser Pro Gly Pro Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala
      5          10          15
Glu Gly Glu Gly Cys Ala Pro Cys Arg Pro Glu Glu Cys Ala Ala Pro
    20          25          30
Arg Gly Cys Leu Ala Gly Arg Val Arg Asp Ala Cys Gly Cys Cys Trp
35          40          45          50
Glu Cys Ala Asn Leu Glu Gly Gln Leu Cys Asp Leu Asp Pro Ser Ala
          55          60          65
His Phe Tyr Gly His Cys Gly Glu Gln Leu Glu Cys Arg Leu Asp Thr
      70          75          80
Gly Gly Asp Leu Ser Arg Gly Glu Val Pro Glu Pro Leu Cys Ala Cys
    85          90          95
Arg Ser Gln Ser Pro Leu Cys Gly Ser Asp Gly His Thr Tyr Ser Gln
    100          105          110
Ile Cys Arg Leu Gln Glu Ala Ala Arg Ala Arg Pro Asp Ala Asn Leu
115          120          125          130
Thr Val Ala His Pro Gly Pro Cys Glu Ser Gly Pro Gln Ile Val Ser
          135          140          145
His Pro Tyr Asp Thr Trp Asn Val Thr Gly Gln Asp Val Ile Phe Gly
    150          155          160
Cys Glu Val Phe Ala Tyr Pro Met Ala Ser Ile Glu Trp Arg Lys Asp
    165          170          175
Gly Leu Asp Ile Gln Leu Pro Gly Asp Asp Pro His Ile Ser Val Gln
    180          185          190
Phe Arg Gly Gly Pro Gln Arg Phe Glu Val Thr Gly Trp Leu Gln Ile
195          200          205          210
Gln Ala Val Arg Pro Ser Asp Glu Gly Thr Tyr Arg Cys Leu Gly Pro
          215          220          225
Met Pro Trp Val Lys Trp Arg Pro Leu Leu Ala
    230          235

```

```

<210> 81
<211> 1406
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..26

```

```

<220>
<221> CDS
<222> 27..689

```

```

<220>
<221> 3'UTR
<222> 690..1406

```

```

<220>

```

&lt;221&gt; polyA\_signal

&lt;222&gt; 1302..1307

&lt;220&gt;

&lt;221&gt; polyA\_site

&lt;222&gt; 1325..1406

&lt;400&gt; 81

```

ccccggaagtg cgcaggcgct ggcaag atg gcg gga ggg gtg cgc ccg ctg cgg      53
                               Met Ala Gly Gly Val Arg Pro Leu Arg
                               -30                               -25

ggc ctc cgc gcc ttg tgt cgc gtg ctg ctc ttc ctt tcg cag ttc tgc      101
Gly Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys
                               -20                               -15                               -10

att ctg tcg ggc ggt gaa agt act gaa atc cca cct tat gtg atg aag      149
Ile Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys
                               -5                               1                               5                               10

tgt ccg agc aat ggt ttg tgt agc agg ctt cct gca gac tgt ata gac      197
Cys Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp
                               15                               20                               25

tgc aca aca aat ttc tcc tgt acc tat ggg aag cct gtc act ttt gac      245
Cys Thr Thr Asn Phe Ser Cys Thr Tyr Gly Lys Pro Val Thr Phe Asp
                               30                               35                               40

tgt gca gtg aaa cca tct gtt acc tgt gtt gat caa gac ttc aaa tcc      293
Cys Ala Val Lys Pro Ser Val Thr Cys Val Asp Gln Asp Phe Lys Ser
                               45                               50                               55

caa aag aac ttc atc att aac atg act tgc aga ttt tgc tgg cag ctt      341
Gln Lys Asn Phe Ile Ile Asn Met Thr Cys Arg Phe Cys Trp Gln Leu
                               60                               65                               70

cct gaa aca gat tac gag tgt acc aac tcc acc agc tgc atg acg gtg      389
Pro Glu Thr Asp Tyr Glu Cys Thr Asn Ser Thr Ser Cys Met Thr Val
75                               80                               85                               90

tcc tgt cct cgg cag cgc tac cct gcc aac tgc acg gtg cgg gac cac      437
Ser Cys Pro Arg Gln Arg Tyr Pro Ala Asn Cys Thr Val Arg Asp His
                               95                               100                               105

gtc cac tgc ttg ggt aac cgt act ttt ccc aaa atg cta tat tgc aat      485
Val His Cys Leu Gly Asn Arg Thr Phe Pro Lys Met Leu Tyr Cys Asn
                               110                               115                               120

tgg act gga ggc tat aag tgg tct acg gct ctg gct cta agc atc acc      533
Trp Thr Gly Tyr Lys Trp Ser Thr Ala Leu Ala Leu Ser Ile Thr
                               125                               130                               135

ctc ggt ggg ttt gga gca gac cgt ttc tac ctg ggc cag tgg cgg gaa      581
Leu Gly Gly Phe Gly Ala Asp Arg Phe Tyr Leu Gly Gln Trp Arg Glu
                               140                               145                               150

ggc ctc ggc aag ctc ttc agc ttc ggt ggc ctg gga ata tgg acg ctg      629
Gly Leu Gly Lys Leu Phe Ser Phe Gly Gly Leu Gly Ile Trp Thr Leu
155                               160                               165                               170

ata gac gtc ctg ctc att gga gtt ggc tat gtt gga cca gca gat ggc      677
Ile Asp Val Leu Leu Ile Gly Val Gly Tyr Val Gly Pro Ala Asp Gly
                               175                               180                               185

tct ttg tac att tagctgtggt gtgtgcttca gaaaggagca gggcttagaa      729
Ser Leu Tyr Ile
                               190

aaagcccttt tgtccgtagg agttgatgtg gtgtgagtga tatatttcta tgtttttaat      789
gtacagcatc tgtactttgt ttgccttgat aaaggtaaga taaatgaaac gctgaactat      849

```

```

gctaactctgg aatttgTTTT tatttgCctg aaatatattt ttttctgtga aaaaattaaa 909
acgtactttaa gccaggagaa tgaattatac agtgattgaa aatccattta attcctatga 969
cttttgTTTT gtattgCcca agtcaaacta catcattgt atctccagcc caaatgtagt 1029
ctgccttgaa aagtctttca gctgtgactg caggaagtgg gagtgTTTT attgttagct 1089
aattgctgtg actgcaggaa gtgggagtgt ttctgttgtt ggctaattga agttattagg 1149
ctcagcttca gtcatgtgta agttttgcag tgtaatacat atgtagtctg gtctgtatat 1209
atgaaaattt gaattaaact gcagaatgtt tatgtctagt tatggtttaa attttcttag 1269
tagtatataa aaggtaagag tactgaaaaa ttaataaaat tgcaagttaa gaaataaaaa 1329
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1389
taaaaaaaaa aaaaaaat
1406

```

```

<210> 82
<211> 221
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..32

```

```

<400> 82
Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg
      -30                -25                -20
Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser
      -15                -10                -5
Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
1          5          10          15
Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys
      20          25          30
Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val
      35          40          45
Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn
      50          55          60
Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys
65          70          75          80
Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr
      85          90          95
Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg
      100         105         110
Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp
      115         120         125
Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp
      130         135         140
Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser
145         150         155         160
Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly
      165         170         175
Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile
      180         185

```

```

<210> 83
<211> 1754
<212> DNA
<213> Homo sapiens

```



<220>  
 <221> 5'UTR  
 <222> 1..117

<220>  
 <221> CDS  
 <222> 118..510

<220>  
 <221> 3'UTR  
 <222> 511..1754

<220>  
 <221> polyA\_signal  
 <222> 1718..1723

<220>  
 <221> polyA\_site  
 <222> 1739..1754

<400> 83  
 tccccggcgcg ccgcccgttgc gctcgccgcgcg ctgcgactga agccccggggcc ctgcgcgcgcg 60  
 gcgggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc gggtcacg 117  
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165  
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu  
 -20 -15 -10  
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213  
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
 -5 1 5  
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
 10 15 20 25  
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 30 35 40  
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
 45 50 55  
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
 75 80 85  
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro  
 90 95 100 105  
 ggc ccc agc tgaccgcccc agccccgcgt gattgcacct gtctgcattc 550  
 Gly Pro Ser  
 acagacattc gggagacggc cttcgtgttc gccatcactg cggccgggcgc cagccacggc 610  
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670  
 cgggccccctc cccggccctc cggcctgccc ggcacccccg gacccccctg ccccgcgggc 730  
 tccccggaag gcagcgccgc ctgggagtg gagggtgcg gcgacgacgt ggacttcggg 790  
 gacgagaagt cgaggctctt tatgsacgcg cggcacaagc ggggacgcg agacatccgc 850  
 gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910

```

accgagtgca aatgccacgg gctgtcgagg tcatgcgcgc tgcgcacctg ctggcagaag 970
ctgcctccat ttgcgcaggt gggcgcgagg ctgctggagc gcttccacgg cgcctcacgc 1030
gtcatgggca ccaacgacgg caaggccctg ctgcccgcgg tccgcacgct caagccgcgg 1090
ggccgagcgg acctcctcta cgccgcccgt tgcggcgact tctgcgcccc caaccgacgc 1150
accggctccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
tgcgacctgc tgtgctgcgg ccgcggggcac cgccaggaga gcgtgcagct cgaagagaac 1270
tgctgtgcc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgcctgtg acccgccggc cggccgctag actgacttcg cgcagcgggtg 1390
gctgcacact gtgggacctc agggcacggc caccggggcg ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gcccaggggc ccagacggcc ccgaaaaggc gctcggggag 1570
cgtttaaagg aactgtaca ggccctccct ccccttgccc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatatat aaaccaccaa aaaaaaaaaa 1750
aaaa
1754

```

```

<210> 84
<211> 131
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..24

```

```

<400> 84
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
      -20      -15      -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5      1      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10      15      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25      30      35      40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45      50      55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60      65      70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
      75      80      85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
      90      95      100
Gly Pro Ser
105

```

```

<210> 85
<211> 1754
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..117

```

```

<220>

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<221> CDS  
 <222> 118..510

<220>  
 <221> 3'UTR  
 <222> 511..1754

<220>  
 <221> polyA\_signal  
 <222> 1718..1723

<220>  
 <221> polyA\_site  
 <222> 1739..1754

<400> 85  
 tccccggccg ccgccgttgc gctcgccgcg ctgcactga agcccgggcc ctgcgcgcgc 60  
 gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117  
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165  
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu  
 -20 -15 -10  
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213  
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro  
 -5 1 5  
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261  
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala  
 10 15 20 25  
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309  
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu  
 30 35 40  
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357  
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe  
 45 50 55  
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405  
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg  
 60 65 70  
 atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453  
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu  
 75 80 85  
 cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501  
 Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro  
 90 95 100 105  
 ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcatte 550  
 Gly Pro Ser  
 acagacattc gggagacggc cttegtgttc gccatcactg cggccggcgc cagccacgcc 610  
 gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670  
 cgggccccctc cccggccctc cggcctgccc ggcacccccg gacccccctg ccccgcgggc 730  
 tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790  
 gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850  
 gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910  
 accgagtgc aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970  
 ctgcctccat ttcgcgaggt gggcgcgcgg ctgctggagc gcttycacgg cgcctcacgc 1030  
 gtcattgggca ccaacgacgg caaggccctg ctgcccgcgg tccgcacgct caagccgcgg 1090  
 ggccgagcgg acctcctcta cgccgccgat tcgcccgaact tctgcgcccc caaccgacgc 1150  
 accggctccc ccggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210

```

tgcgacctgc tgtgctgcgg ccgcggggcac cgccaggaga gcgtgcagct cgaagagaac 1270
tgccctgtgcc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgacctgtg acccgccgcc cggccgctag actgacttcg cgcagcgggtg 1390
gctcgacact gtgggacctc agggcaccgg caccgggccc ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttgag 1510
aggaacgccc acccacgaag gccagggcg ccagacggcc ccgaaaaggc gctcggggag 1570
cgtttaaagg acactgtaca ggccctccct ccccttggcc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatatatt aaaccaccaa aaaaaaaaaa 1750
aaaaa 1754

```

```

<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..24

```

```

<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
      -20                      -15                      -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5                      1                      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10                      15                      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25                      30                      35                      40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45                      50                      55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60                      65                      70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
      75                      80                      85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
      90                      95                      100
Gly Pro Ser
105

```

```

<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..151

```

```

<220>
<221> CDS
<222> 152..655

```

```

<220>
<221> 3'UTR

```

&lt;222&gt; 656..1431

&lt;220&gt;

&lt;221&gt; polyA\_signal

&lt;222&gt; 1399..1404

&lt;220&gt;

&lt;221&gt; polyA\_site

&lt;222&gt; 1416..1431

&lt;400&gt; 87

```

aattttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa 60
gcccaaacca agggccccag agaggtcccc caggcccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                               Met Leu Phe Arg Leu Ser Glu
                               1           5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
          10           15           20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
          25           30           35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
          40           45           50           55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
          60           65           70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
          75           80           85
gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
          90           95           100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
          105           110           115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
          120           125           130           135
tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
          140           145           150
agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
          155           160           165
aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr
tccccagaaa ccactctat cctcaccctg ttttgtgctc ttcccctcgc ctgctagggc 765
tgcggttct gacttctaga agactaaggc tggctctgtgt ttgcttggtt gccaccttt 825
ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccaccctgc cagtcattcc 885
tccattcacc cagcgggagg tgggatgtga gacagccac attggaaaat ccagaaaacc 945
gggaacaggg atttgccctt cacaattcta ctccccagat cctctcccct ggacacagga 1005
gaccacagg gcaggacct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065
cttagatcct tttctacca ctttctatg gaggattcca agtcaccact tctctaccg 1125

```

```

gcttctacca gggccagga ctaaggcgtt tttctccata gcctcaacat tttgggaatc 1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tggtgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccaggtt ttccttgctc ccagctgct ctgccccctt ccccttcttc 1365
cctgactcca ggcctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa                                     1431

```

```

<210> 88
<211> 168
<212> PRT
<213> Homo sapiens

```

```

<400> 88
Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
1          5          10          15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
          20          25          30
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
          35          40          45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
          50          55          60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65          70          75          80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
          85          90          95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
          100          105          110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
          115          120          125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
          130          135          140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145          150          155          160
Pro Ser Pro Ser Glu Pro Gly Thr
          165

```

```

<210> 89
<211> 1431
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..151

```

```

<220>
<221> CDS
<222> 152..655

```

```

<220>
<221> 3'UTR
<222> 656..1431

```

```

<220>
<221> polyA_signal

```

&lt;222&gt; 1399..1404

&lt;220&gt;

&lt;221&gt; polyA\_site

&lt;222&gt; 1416..1431

&lt;400&gt; 89

```

aatttttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa 60
gccccaaacca aggccccccag agaggtcccc caggccccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                               Met Leu Phe Arg Leu Ser Glu
                               1           5

cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
      10           15           20

gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
      25           30           35

cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
      40           45           50           55

tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
      60           65           70

ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
      75           80           85

gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
      90           95           100

gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
      105           110           115

ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
      120           125           130           135

tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
      140           145           150

agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
      155           160           165

aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
Thr

tccccagaaa ccactctat cctcaccctg ttttgtgctc ttcccctcgc ctgctagggc 765
tgcggttctt gacttctaga agactaaggc tgggtctgtgt ttgcttggtt gccaccttt 825
ggctgatacc cagagaacct gggcacttgc tgcttgatgc ccaccctcgc cagtcattcc 885
tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc 945
gggaacaggg atttgccctt cacaattcta ctcccagat cctctcccct ggacacagga 1005
gaccacagg gcaggacctt aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065
cttagatcct tttctaccca ctttcctatg gaggattcca agtcaccact tctctaccg 1125
gcttctacca gggccagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tgttgcgttt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccaggtt ttccttgtcc ccagctgct ctgccccttt ccccttcttc 1365

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cctgactcca ggcctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425  
 aaaaaa 1431

<210> 90  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
 Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser  
 1 5 10 15  
 Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg  
 20 25 30  
 Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg  
 35 40 45  
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln  
 50 55 60  
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr  
 65 70 75 80  
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu  
 85 90 95  
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser  
 100 105 110  
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu  
 115 120 125  
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp  
 130 135 140  
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg  
 145 150 155 160  
 Pro Ser Pro Ser Glu Pro Gly Thr  
 165

<210> 91  
 <211> 1417  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..47

<220>  
 <221> CDS  
 <222> 48..1301

<220>  
 <221> 3'UTR  
 <222> 1302..1417

<220>  
 <221> polyA\_signal  
 <222> 1360..1365

<220>  
 <221> polyA\_site



&lt;222&gt; 1402..1417

&lt;400&gt; 91

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ctcctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct      56
                                     Met Pro Ser

tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc      104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20                               -15                -10                -5
cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca      152
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
                               1                5                10
gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc      200
Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
                               15                20                25
ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac      248
Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
                               30                35                40
cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca      296
Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
45                               50                55                60
gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa      344
Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
                               65                70                75
atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag      392
Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
                               80                85                90
atc cat gaa ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac      440
Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
                               95                100                105
agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc      488
Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
                               110                115                120
ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac      536
Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
125                130                135                140
tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa      584
Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
                               145                150                155
cag atc aac gat tac gtg gag aag ggt act caa ggg aaa att gtg gat      632
Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
                               160                165                170
ttg gtc aag gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac      680
Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr
                               175                180                185
atc ttc ttt aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc      728
Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr
190                195                200
gag gaa gag gac ttc cac gtg gac cag gcg acc acc gtg aag gtg cct      776
Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val Lys Val Pro
205                210                215                220
atg atg aag cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg      824
Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu
                               225                230                235
tcc agc tgg gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc      872
Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile

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      240      245      250
ttc ttc ctg cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc 920
Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu
      255      260      265
acc cac gat atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct 968
Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser
      270      275      280
gcc agc tta cat tta ccc aaa ctg tcc att act gga acc tat gat ctg 1016
Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu
      285      290      295      300
aag agc gtc ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg 1064
Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly
      305      310      315
gct gac ctc tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag 1112
Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
      320      325      330
gcc gtg cat aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct 1160
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala
      335      340      345
gct ggg gcc atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag 1208
Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu
      350      355      360
gtc aag ttc aac aaa ccc ttt gtc ttc tta atg att gaa caa aat acc 1256
Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr
      365      370      375      380
aag tct ccc ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa 1301
Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys
      385      390      395
taactgcctc tcgctcctca acccctcccc tccatccctg gccccctccc tggatgacat 1361
taaagaaggg ttgagctggt cctgctctgc atgtgactgc aaaaaaaaaa aaaaaa 1417

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<210> 92  
 <211> 418  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..24

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<400> 92
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
      -20      -15      -10
Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
      -5      1      5
Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
      10      15      20
Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
      25      30      35      40
Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
      45      50      55
Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
      60      65      70
His Asp Glu Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro
      75      80      85

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Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn  
 90 95 100  
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu  
 105 110 115 120  
 Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys  
 125 130 135  
 Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu  
 140 145 150  
 Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys  
 155 160 165  
 Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu  
 170 175 180  
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
 185 190 195 200  
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val  
 205 210 215  
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys  
 220 225 230  
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala  
 235 240 245  
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu  
 250 255 260  
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp  
 265 270 275 280  
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr  
 285 290 295  
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
 300 305 310  
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys  
 315 320 325  
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly  
 330 335 340  
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile  
 345 350 355 360  
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu  
 365 370 375  
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr  
 380 385 390  
 Gln Lys

<210> 93  
 <211> 1115  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..277

<220>  
 <221> CDS  
 <222> 278..733

<220>  
 <221> 3'UTR

<222> 734..1115

<220>

<221> polyA\_signal

<222> 1072..1077

<220>

<221> polyA\_site

<222> 1101..1115

<400> 93

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ctcttttgcgc taacagacag cagcgacttt aggctggata atagtcaa at tcttacctcg 60
ctcttttcaact gctagtaaga tcagattgcg tttcttttcag ttactcttca atcgccagtt 120
tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaaaca aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
                                Met His Phe Gly Leu Leu
                                -15
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
-10 -5 1
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
5 10 15 20
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
25 30 35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
40 45 50
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
55 60 65
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
70 75 80
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
85 90 95 100
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
105 110 115
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
120 125 130
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggg 783
Ala Ile
ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
actccgcaat caaccaaggt tcccagcctt tttgtttaca aagaaggaac aaatgatggg 903
tggaagaatg cggctcatat ttaccaagtc tttctgaacg ccttctgcat tcatgcatcc 963
atgttctttc taggattgga tagcatttca tgcctatggt aatatttgtg cttttggcat 1023
ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
atattttacat gcataggaaa aaaaaaaaaa aa 1115

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<210> 94

<211> 152  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..19

<400> 94  
 Met His Phe Gly Leu Leu Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro  
                   -15                  -10                  -5  
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp  
                   1                  5                  10  
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys  
           15                  20                  25  
 Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn  
 30                  35                  40                  45  
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly  
                   50                  55                  60  
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr  
           65                  70                  75  
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys  
           80                  85                  90  
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr  
           95                  100                  105  
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser  
 110                  115                  120                  125  
 Ser Met Val Asp Ala Trp Ala Ile  
                   130

<210> 95  
 <211> 1307  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..252

<220>  
 <221> CDS  
 <222> 253..744

<220>  
 <221> 3'UTR  
 <222> 745..1307

<220>  
 <221> polyA\_signal  
 <222> 1269..1274

<220>  
 <221> polyA\_site  
 <222> 1292..1307

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<400> 95
ctcttttgctc taacagacag cagcgacttt aggcctggata atagtcaa at tctttacctcg 60
ctcttttcaact gctagtaaga tcagattgcg tttcttttcag ttactcttca atcgccagtt 120
tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291
      Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala
      -25 -20 -15
tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339
Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp
      -10 -5 1
tct gag gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca 387
Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro
      5 10 15
cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat ggc 435
Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly
      20 25 30
cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga 483
Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg
      35 40 45 50
cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga 531
Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg
      55 60 65
ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca 579
Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala
      70 75 80
aac agg att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc 627
Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys
      85 90 95
ttt ttg gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat 675
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
      100 105 110
ttt tat aac aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga 723
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
      115 120 125 130
tgc ctg ggc aat caa caa ttt tgagacactg gaacaatgca agaacatttg 774
Cys Leu Gly Asn Gln Gln Phe
      135
tgaagatggt ccgaatggtt tccaggtgga taattatgga acccagctca atgctgtgaa 834
taactccctg actccgcaat caaccaaggt tcccagcctt tttgaatttc acggtccctc 894
atgggtgtctc actccagcag acagaggatt gtgtcgtgcc aatgagaaca gattctacta 954
caatttcagtc attgggaaat gccgccatt taagtacagt ggatgtgggg gaaatgaaaa 1014
caattttact tccaaacaag aatgtctgag ggcattgtaa aaagggtttca tccaaagaat 1074
atcaaaaagga ggcctaatta aaaccaaag aaaaagaaag aagcagagag tgaaaatagc 1134
atatgaagaa atttttgtta aaaatatgtg aatttgttat agcaatgtaa cattaattct 1194
actaaatatt ttatatgaaa tgtttcacta tgattttcta tttttcttct aaaatgcttt 1254
taattaatat gttcattaa ttttctatgc ttattgcaaa aaaaaaaaaa aaa 1307

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<210> 96

<211> 164

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..28

<400> 96

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Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
      -25                      -20                      -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
      -10                      -5                      1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5      10      15      20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
      25      30      35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
      40      45      50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
      55      60      65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile
      70      75      80
Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu
85      90      95      100
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
      105      110      115
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
      120      125      130
Asn Gln Gln Phe
      135

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<210> 97

<211> 1855

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..117

<220>

<221> CDS

<222> 118..504

<220>

<221> 3'UTR

<222> 505..1855

<220>

<221> polyA\_signal

<222> 1819..1824

<220>

<221> polyA\_site

<222> 1840..1855

<400> 97

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tccccggccg ccgccgttgc gctcgccgcg ctgcactga agccccgggccc ctgcgcgcgc 60
gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165

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Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
      -20      -15      -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5      1      5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10      15      20      25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      30      35      40
ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45      50      55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60      65      70
atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
      75      80      85
tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
90      95      100      105
gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554
Ala
cctcccaggc ccctggggca gccctccgc cgcaggtttc aggtcccagg cccagctga 614
ccgccccagc ccgcgctgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
cgtgttcgcc atcactgcgg ccggcgccag ccacgcgctc acgcaggcct gttctatggg 734
cgagctgctg cagtgcggct gccaggcgcc ccgcgggcgg gcccctcccc ggccctccgg 794
cctgccccgg acccccgga cccctggccc cgcgggctcc ccggaaggca gcgcgcctg 854
ggagtgggga ggctgcggcg acgacgtgga cttcggggac gagaagtcga ggctctttat 914
ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974
cgaggcgggc aggtctggcg tgcggagcca cacgcgcacc gagtgc aaat gccacgggct 1034
gtcgggatca tgcgcgtgc gcacctgctg gcagaagctg cctccatttc gcgagggtgg 1094
cgcgcggctg ctggagcgct tccacggcgc ctcacgcgtc atgggcacca acgacggcaa 1154
ggccctgctg cccgcgctcc gcacgtcaa gccgcggggc cgagcggacc tccctacgc 1214
cgccgattcg cccgacttct gcgcccccaa ccgacgcacc ggctcccccg gcacgcgcgg 1274
tcgcgcctgc aatagcagcg ccccggaact cagcggtgc gacctgctgt gctgcggcgg 1334
cgggcacgcg caggagagcg tgcagctcga agagaactgc ctgtgccgct tccactggtg 1394
ctgcgtagta cagtgccacc gctgccgtgt gcgcaaggag ctcagcctct gectgtgacc 1454
cgccgccccg ccgctagact gacttcgcgc agcgggtggct cgcacctgtg ggacctcagg 1514
gcaccggcac cgggcgcctc tcgcgcgtcg agcccagcct ctccctgcca aagcccaact 1574
cccagggtc tggaaatggt gaggcgagg gcttgagagg aacgcccacc cacgaaggcc 1634
cagggcgcca gacggccccg aaaaggcgct cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc cttggcctct aggaggaaac agtttttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tcccagaac tgctggccac aggatggtgg gtgagggttag 1814
tatcaataaa gatatttaaa ccaccaaaaa aaaaaaaaaa a 1855

```

<210> 98  
 <211> 129  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL



<222> 1..24

<400> 98

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Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
      -20                      -15                      -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5                      1                      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10                      15                      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25                      30                      35                      40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45                      50                      55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60                      65                      70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
      75                      80                      85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
      90                      95                      100
Ala
105

```

<210> 99

<211> 667

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..94

<220>

<221> CDS

<222> 95..613

<220>

<221> 3'UTR

<222> 614..667

<220>

<221> polyA\_signal

<222> 636..641

<220>

<221> polyA\_site

<222> 652..667

<400> 99

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ctctgcaaat ccaggacaca cattgtgctc cgcgctccac taaaggcttg agtgggcact 60
gttccatctc aacagcccct gttttggaaa ggac atg att gtc aag ggg gtg gcc 115
      Met Ile Val Lys Gly Val Ala
                        1                      5
tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser
      10                      15                      20

```

```

tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val
25 30 35
gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile
40 45 50 55
ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys
60 65 70
acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile
75 80 85
aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr
90 95 100
gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu
105 110 115
tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met
120 125 130 135
gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val
140 145 150
gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys
155 160 165
caa acc act gtg aaa aat tagcttttgaa agctatatct ggaataaata 643
Gln Thr Thr Val Lys Asn
170
tcttttcgcaa aaaaaaaaaa aaaa 667

```

```

<210> 100
<211> 173
<212> PRT
<213> Homo sapiens

```

```

<400> 100
Met Ile Val Lys Gly Val Ala Ser Arg Thr Val Val Ser Arg Pro Phe
1 5 10 15
Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
20 25 30
Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn
35 40 45
Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val
50 55 60
Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile
65 70 75 80
His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His
85 90 95
Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro
100 105 110
Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp
115 120 125
Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser

```

```

      130              135              140
Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr
145              150              155              160
Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn
      165              170

```

```

<210> 101
<211> 1062
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..153

```

```

<220>
<221> CDS
<222> 154..639

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```

<220>
<221> 3'UTR
<222> 640..1062

```

```

<220>
<221> polyA_signal
<222> 1023..1028

```

```

<220>
<221> polyA_site
<222> 1047..1062

```

```

<400> 101
attggtgtat ggctttgcag caataactga tggctgtttc ccctcctgct ttatctttca 60
gttaatgacc agccacggcg tccctgctgt gagctctggc cgctgccttc cagggctccc 120
gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174
              Met Ala Cys Trp Pro Gln Leu
              1              5
agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222
Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys
      10              15              20
cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg 270
Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu
      25              30              35
atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat 318
Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His
      40              45              50              55
ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag 366
Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln
      60              65              70
ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414
Gly Ile Ile Cys Asn Ala Asn Asn Pro Cys Phe Arg Tyr Pro Thr Pro
      75              80              85
ggg gag gct ccc gga gtt gtt gga aac ttt aac aaa tcc att gtg gct 462
Gly Glu Ala Pro Gly Val Val Gly Asn Phe Asn Lys Ser Ile Val Ala
      90              95              100

```

```

cgc ctg ttc tca gat gct cgg agg ctt ctt tta tac agc cag aaa gac      510
Arg Leu Phe Ser Asp Ala Arg Leu Leu Leu Tyr Ser Gln Lys Asp
      105                      110                      115
acc agc atg aag gac atg cgc aaa gtt ctg aga aca tta cag cag atc      558
Thr Ser Met Lys Asp Met Arg Lys Val Leu Arg Thr Leu Gln Gln Ile
      120                      125                      130                      135
aag aaa tcc agc tca aga ggg gac aaa cgc cat ttc ctc aac tgg cag      606
Lys Lys Ser Ser Ser Arg Gly Asp Lys Arg His Phe Leu Asn Trp Gln
                      140                      145                      150
aag gga ctg aag cct ctc cct caa gcc ctt tta taggggtcct cattgtcagg      659
Lys Gly Leu Lys Pro Leu Pro Gln Ala Leu Leu
      155                      160
cctctaagcc caagccaagc catcgcatcc cctgtgactt gcacatatac gcccagatgg      719
cctgaagtaa ctgaagaatc acaaaagaag tgaaaaggcc ctgcctcgcc ttaactgatg      779
acgttccacc attgtgattt gttcctgccc caccttaact gagtgattaa ccctgtgaat      839
ttcctttctcc tggctcagaa gctccccccac tgagcacctt gtgaccccct gcccctgccc      899
accagagaac aacccccctt gactgtaatt ttccattacc ttcccaaata ctataaaaacg      959
gccccacccc tatctccctt tgctgactct cttttcggaac tcagcccacc tgcagccagg      1019
tgaaaaaaaac agctttattg ctcacacaaa aaaaaaaaaaa aaa                        1062

```

&lt;210&gt; 102

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 102

```

Met Ala Cys Trp Pro Gln Leu Arg Leu Leu Leu Trp Lys Asn Leu Thr
1          5          10          15
Phe Arg Arg Arg Gln Thr Cys Gln Leu Leu Leu Glu Val Ala Trp Pro
      20          25          30
Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro
      35          40          45
Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala
      50          55          60
Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro
      65          70          75          80
Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn
      85          90          95
Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu
      100          105          110
Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val
      115          120          125
Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Arg Gly Asp Lys
      130          135          140
Arg His Phe Leu Asn Trp Gln Lys Gly Leu Lys Pro Leu Pro Gln Ala
      145          150          155          160
Leu Leu

```

&lt;210&gt; 103

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; 5'UTR

<222> 1..149

<220>

<221> CDS

<222> 150..392

<220>

<221> 3'UTR

<222> 393..933

<220>

<221> polyA\_site

<222> 63..933

<400> 103

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aaaccctcag ggacctggta tagacgcaga atctgtttca cacaacaact gctatttgaa 60
ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
cagatgtgta cggatgaaaa tacagtggag atg agt cag aaa ccg gcc aag gag 173
                               Met Ser Gln Lys Pro Ala Lys Glu
                               1           5
ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
   10           15           20
cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
   25           30           35           40
gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
           45           50           55
gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
           60           65           70
aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
Lys Ile Arg Pro Thr Pro Lys Lys Lys
           75           80
ytgaatgaac aacctcggct cctggactca ttgcttcaca acccatctac cctgggatga 472
agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
gctcatggtc cccatggcat gggggcctca gggcagcctg cctggagtag tttgaagatg 592
tcatcccatg gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
atccttcacg ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
tggaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
gcgtgggtggc gggcgccctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832
gaacctggga ggcggagctt gcagtgagcc gagatcgcac cactgcactc cagcctgggc 892
gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933

```

<210> 104

<211> 81

<212> PRT

<213> Homo sapiens

<400> 104

```

Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
1           5           10           15
Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
           20           25           30

```

Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys  
           35                  40                  45  
 Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala  
       50                  55                  60  
 Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys  
 65                  70                  75                  80  
 Lys

<210> 105  
 <211> 1187  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> 1..34

<220>  
 <221> CDS  
 <222> 35..1069

<220>  
 <221> 3'UTR  
 <222> 1070..1187

<220>  
 <221> polyA\_signal  
 <222> 1146..1151

<220>  
 <221> polyA\_site  
 <222> 1172..1187

<400> 105  
 accactttgg tagtgccagt gtgactcatc caca atg att tct cca gtg ctc atc 55  
                                   Met Ile Ser Pro Val Leu Ile  
   -15  
 ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt 103  
 Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys  
       -10                  -5                  1                  5  
 ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca 151  
 Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr  
                   10                  15                  20  
 ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199  
 Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr  
           25                  30                  35  
 gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247  
 Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu  
       40                  45                  50  
 tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct 295  
 Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala  
       55                  60                  65  
 gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc 343  
 Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro  
 70                  75                  80                  85

```

aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct 391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala
90 95 100
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct 439
Asp Ser Ala Lys Cys Thr Glu Glu Lys Trp Ser Pro Glu Leu Pro
105 110 115
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca 487
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala
120 125 130
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg 535
Thr Leu Arg Val Tyr Lys Pro Ser Ala Gly Asn Asn Ser Leu Tyr Arg
135 140 145
gac aca gca gtt ttt gaa tgt ttg cca caa cat gcg atg ttt gga aat 583
Asp Thr Ala Val Phe Glu Cys Leu Pro Gln His Ala Met Phe Gly Asn
150 155 160 165
gat aca att acc tgc acg aca cat gga aat tgg act aaa tta cca gaa 631
Asp Thr Ile Thr Cys Thr Thr His Gly Asn Trp Thr Lys Leu Pro Glu
170 175 180
tgc agg gaa gta aaa tgc cca ttc cca tca aga cca gac aat gga ttt 679
Cys Arg Glu Val Lys Cys Pro Phe Pro Ser Arg Pro Asp Asn Gly Phe
185 190 195
gtg aac tat cct gca aaa cca aca ctt tat tac aag gat aaa gcc aca 727
Val Asn Tyr Pro Ala Lys Pro Thr Leu Tyr Tyr Lys Asp Lys Ala Thr
200 205 210
ttt ggc tgc cat gat gga tat tct ctg gat ggc ccg gaa gaa ata gaa 775
Phe Gly Cys His Asp Gly Tyr Ser Leu Asp Gly Pro Glu Glu Ile Glu
215 220 225
tgt acc aaa ctg gga aac tgg tct gcc atg cca agt tgt aaa gca tct 823
Cys Thr Lys Leu Gly Asn Trp Ser Ala Met Pro Ser Cys Lys Ala Ser
230 235 240 245
tgt aaa gta cct gtg aaa aaa gcc act gtg gtg tac caa gga gag aga 871
Cys Lys Val Pro Val Lys Lys Ala Thr Val Val Tyr Gln Gly Glu Arg
250 255 260
gta aag att cag gaa aaa ttt aag aat gga atg cta cat ggt gat aaa 919
Val Lys Ile Gln Glu Lys Phe Lys Asn Gly Met Leu His Gly Asp Lys
265 270 275
gtt tct ttc ttc tgc aaa aat aag gaa aag aag tgt agc tat aca gag 967
Val Ser Phe Phe Cys Lys Asn Lys Glu Lys Lys Cys Ser Tyr Thr Glu
280 285 290
gat gct cag tgt ata gat ggc act atc gaa gtc ccc aaa tgc ttc aag 1015
Asp Ala Gln Cys Ile Asp Gly Thr Ile Glu Val Pro Lys Cys Phe Lys
295 300 305
gaa cac agt tct ctg gct ttt tgg aaa act gat gca tcc gat gta aag 1063
Glu His Ser Ser Leu Ala Phe Trp Lys Thr Asp Ala Ser Asp Val Lys
310 315 320 325
cca tgc taaggtggtt ttcagattcc acataaaatg tcacacttgt ttcttggtca 1119
Pro Cys
tccaaggaac ctaattgaaa tttaaaaata aagctactga atttattgcc gcaaaaaaaaa 1179
aaaaaaaa 1187

```

```

<210> 106
<211> 345
<212> PRT
<213> Homo sapiens

```

&lt;220&gt;

&lt;221&gt; SIGNAL

&lt;222&gt; 1..19

&lt;400&gt; 106

```

Met Ile Ser Pro Val Leu Ile Leu Phe Ser Ser Phe Leu Cys His Val
              -15                      -10                      -5
Ala Ile Ala Gly Arg Thr Cys Pro Lys Pro Asp Asp Leu Pro Phe Ser
              1                      5                      10
Thr Val Val Pro Leu Lys Thr Phe Tyr Glu Pro Gly Glu Glu Ile Thr
    15              20              25
Tyr Ser Cys Lys Pro Gly Tyr Val Ser Arg Gly Gly Met Arg Lys Phe
30              35              40              45
Ile Cys Pro Leu Thr Gly Leu Trp Leu Ile Asn Thr Leu Lys Cys Thr
              50              55              60
Pro Arg Val Cys Pro Phe Ala Gly Ile Leu Glu Asn Gly Ala Val Arg
              65              70              75
Tyr Thr Thr Phe Glu Tyr Pro Asn Thr Ile Ser Phe Ser Cys Asn Thr
    80              85              90
Gly Phe Tyr Leu Asn Gly Ala Asp Ser Ala Lys Cys Thr Glu Glu Gly
    95              100              105
Lys Trp Ser Pro Glu Leu Pro Val Cys Ala Pro Ile Ile Cys Pro Pro
110              115              120              125
Pro Ser Ile Pro Thr Phe Ala Thr Leu Arg Val Tyr Lys Pro Ser Ala
              130              135              140
Gly Asn Asn Ser Leu Tyr Arg Asp Thr Ala Val Phe Glu Cys Leu Pro
              145              150              155
Gln His Ala Met Phe Gly Asn Asp Thr Ile Thr Cys Thr Thr His Gly
              160              165              170
Asn Trp Thr Lys Leu Pro Glu Cys Arg Glu Val Lys Cys Pro Phe Pro
              175              180              185
Ser Arg Pro Asp Asn Gly Phe Val Asn Tyr Pro Ala Lys Pro Thr Leu
190              195              200              205
Tyr Tyr Lys Asp Lys Ala Thr Phe Gly Cys His Asp Gly Tyr Ser Leu
              210              215              220
Asp Gly Pro Glu Glu Ile Glu Cys Thr Lys Leu Gly Asn Trp Ser Ala
              225              230              235
Met Pro Ser Cys Lys Ala Ser Cys Lys Val Pro Val Lys Lys Ala Thr
              240              245              250
Val Val Tyr Gln Gly Glu Arg Val Lys Ile Gln Glu Lys Phe Lys Asn
              255              260              265
Gly Met Leu His Gly Asp Lys Val Ser Phe Phe Cys Lys Asn Lys Glu
270              275              280              285
Lys Lys Cys Ser Tyr Thr Glu Asp Ala Gln Cys Ile Asp Gly Thr Ile
              290              295              300
Glu Val Pro Lys Cys Phe Lys Glu His Ser Ser Leu Ala Phe Trp Lys
              305              310              315
Thr Asp Ala Ser Asp Val Lys Pro Cys
              320              325

```

&lt;210&gt; 107

&lt;211&gt; 1520

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



<220>  
 <221> 5'UTR  
 <222> 1..15

<220>  
 <221> CDS  
 <222> 16..1449

<220>  
 <221> 3'UTR  
 <222> 1450..1520

<220>  
 <221> polyA\_signal  
 <222> 1483..1488

<220>  
 <221> polyA\_site  
 <222> 1505..1520

<400> 107

```

cttttttttg acaag atg gcg gca gga ggc agt ggc gtt ggt ggg aag cgc      51
      Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg
              1              5              10
agc tcg aaa agc gat gcc gat tct ggt ttc ctg ggg ctg cgg ccc act      99
Ser Ser Lys Ser Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr
      15              20              25
tcg gtg gac cca gcg ctg agg cgg cgg cgg cga ggc cca aga aat aag      147
Ser Val Asp Pro Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys
      30              35              40
aag cgg ggc tgg cgg cgg ctt gct cag gag ccg ctg ggg ctg gag gtt      195
Lys Arg Gly Trp Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val
      45              50              55              60
gac cag ttc ctg gaa gac gtg cgg cta cag gag cgc acg agc ggt ggc      243
Asp Gln Phe Leu Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly
      65              70              75
ttg ttg tca gag gcc cca aat gaa aaa ctc ttc ttc gtg gac act ggc      291
Leu Leu Ser Glu Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly
      80              85              90
tcc aag gaa aaa ggg ctg aca aag aag aga acc aaa gtc cag aag aag      339
Ser Lys Glu Lys Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys
      95              100              105
tca ctg ctt ctc aag aaa ccc ctt cgg gtt gac ctc atc ctc gag aac      387
Ser Leu Leu Leu Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn
      110              115              120
aca tcc aaa gtc cct gcc ccc aaa gac gtc ctc gcc cac cag gtc ccc      435
Thr Ser Lys Val Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro
      125              130              135              140
aac gcc aag aag ctc agg cgg aag gag cag cta tgg gag aag ctg gcc      483
Asn Ala Lys Lys Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala
      145              150              155
aag cag ggc gag ctg ccc cgg gag gtg cgc agg gcc cag gcc cgg ctc      531
Lys Gln Gly Glu Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu
      160              165              170
ctc aac cct tct gca aca agg gcc aag ccc ggg ccc cag gac acc gta      579

```

Leu	Asn	Pro	Ser	Ala	Thr	Arg	Ala	Lys	Pro	Gly	Pro	Gln	Asp	Thr	Val		
		175					180					185					
gag	cgg	ccc	ttc	tac	gac	ctc	tgg	gcc	tca	gac	aac	ccc	ctg	gac	agg	627	
Glu	Arg	Pro	Phe	Tyr	Asp	Leu	Trp	Ala	Ser	Asp	Asn	Pro	Leu	Asp	Arg		
		190					195				200						
ccg	ttg	gtt	ggc	cag	gat	gag	ttt	ttc	ctg	gag	cag	acc	aag	aag	aaa	675	
Pro	Leu	Val	Gly	Gln	Asp	Glu	Phe	Phe	Leu	Glu	Gln	Thr	Lys	Lys	Lys		
		205				210				215					220		
gga	gtg	aag	cgg	cca	gca	cgc	ctg	cac	acc	aag	ccg	tcc	cag	gca	ccc	723	
Gly	Val	Lys	Arg	Pro	Ala	Arg	Leu	His	Thr	Lys	Pro	Ser	Gln	Ala	Pro		
				225					230					235			
gcc	gtg	gag	gtg	gcg	cct	gcc	gga	gct	tcc	tac	aat	cca	tcc	ttt	gaa	771	
Ala	Val	Glu	Val	Ala	Pro	Ala	Gly	Ala	Ser	Tyr	Asn	Pro	Ser	Phe	Glu		
				240				245					250				
gac	cac	cag	acc	ctg	ctc	tca	gcg	gcc	cac	gag	gtg	gag	ttg	cag	cgg	819	
Asp	His	Gln	Thr	Leu	Leu	Ser	Ala	Ala	His	Glu	Val	Glu	Leu	Gln	Arg		
		255					260					265					
cag	aag	gag	gcg	gag	aag	ctg	gag	cgg	cag	ctg	gcc	ctg	ccc	gcc	acg	867	
Gln	Lys	Glu	Ala	Glu	Lys	Leu	Glu	Arg	Gln	Leu	Ala	Leu	Pro	Ala	Thr		
		270				275					280						
gag	cag	gcc	gcc	acc	cag	gag	tcc	aca	ttc	cag	gag	ctg	tgc	gag	ggg	915	
Glu	Gln	Ala	Ala	Thr	Gln	Glu	Ser	Thr	Phe	Gln	Glu	Leu	Cys	Glu	Gly		
		285				290				295					300		
ctg	ctg	gag	gag	tcg	gat	ggt	gag	ggg	gag	cca	ggc	cag	ggc	gag	ggg	963	
Leu	Leu	Glu	Glu	Ser	Asp	Gly	Glu	Gly	Glu	Pro	Gly	Gln	Gly	Glu	Gly		
				305					310					315			
ccg	gag	gct	ggg	gat	gcc	gag	gtc	tgt	ccc	acg	ccc	gcc	cgc	ctg	gcc	1011	
Pro	Glu	Ala	Gly	Asp	Ala	Glu	Val	Cys	Pro	Thr	Pro	Ala	Arg	Leu	Ala		
			320					325					330				
acc	aca	gag	aag	aag	acg	gag	cag	cag	cgg	cgg	cgg	gag	aag	gct	gtg	1059	
Thr	Thr	Glu	Lys	Lys	Thr	Glu	Gln	Gln	Arg	Arg	Arg	Glu	Lys	Ala	Val		
		335					340					345					
cac	agg	ctg	cgg	gta	cag	cag	gcc	gcg	ttg	cgg	gcc	gcc	cgg	ctc	cgg	1107	
His	Arg	Leu	Arg	Val	Gln	Gln	Ala	Ala	Leu	Arg	Ala	Ala	Arg	Leu	Arg		
		350				355					360						
cac	cag	gag	ctg	ttc	cgg	ctg	cgc	ggg	atc	aag	gcc	cag	gtg	gcc	ctg	1155	
His	Gln	Glu	Leu	Phe	Arg	Leu	Arg	Gly	Ile	Lys	Ala	Gln	Val	Ala	Leu		
		365			370				375					380			
agg	ctg	gcg	gag	ctg	gcg	cgg	cgg	cag	agg	cgg	cgg	cag	gcg	cgg	cgg	1203	
Arg	Leu	Ala	Glu	Leu	Ala	Arg	Arg	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Arg		
				385					390					395			
gag	gct	gag	gct	gac	aag	ccc	cga	agg	ctg	ggg	cgg	ctc	aag	tac	cag	1251	
Glu	Ala	Glu	Ala	Asp	Lys	Pro	Arg	Arg	Leu	Gly	Arg	Leu	Lys	Tyr	Gln		
			400					405					410				
gca	cct	gac	atc	gac	gtg	cag	ctg	agc	tcg	gag	ctg	aca	gac	tcg	ctc	1299	
Ala	Pro	Asp	Ile	Asp	Val	Gln	Leu	Ser	Ser	Glu	Leu	Thr	Asp	Ser	Leu		
		415					420					425					
agg	acc	ctg	aag	ccc	gag	ggc	aac	atc	ctt	cga	gac	cgg	ttc	aag	agc	1347	
Arg	Thr	Leu	Lys	Pro	Glu	Gly	Asn	Ile	Leu	Arg	Asp	Arg	Phe	Lys	Ser		
		430				435					440						
ttc	cag	agg	agg	aat	atg	atc	gag	cct	cga	gag	aga	gcc	aag	ttc	aaa	1395	
Phe	Gln	Arg	Arg	Asn	Met	Ile	Glu	Pro	Arg	Glu	Arg	Ala	Lys	Phe	Lys		
		445			450				455					460			
cgc	aag	tac	aag	gtg	aag	ctg	gtg	gag	aag	cgg	gcg	ttc	cgt	gag	atc	1443	
Arg	Lys	Tyr	Lys	Val	Lys	Leu	Val	Glu	Lys	Arg	Ala	Phe	Arg	Glu	Ile		

465 470 475  
 cag ttg tagctgccat cagatgccgg agactcgccc ttcaataaaa aatctcttct 1499  
 Gln Leu  
 agctcaaaaa aaaaaaaaaa a 1520

<210> 108  
 <211> 478  
 <212> PRT  
 <213> Homo sapiens

<400> 108  
 Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser  
 1 5 10 15  
 Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro  
 20 25 30  
 Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp  
 35 40 45  
 Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu  
 50 55 60  
 Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu  
 65 70 75 80  
 Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys  
 85 90 95  
 Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu  
 100 105 110  
 Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val  
 115 120 125  
 Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys  
 130 135 140  
 Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu  
 145 150 155 160  
 Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu Leu Asn Pro Ser  
 165 170 175  
 Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val Glu Arg Pro Phe  
 180 185 190  
 Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg Pro Leu Val Gly  
 195 200 205  
 Gln Asp Glu Phe Phe Leu Glu Gln Thr Lys Lys Lys Gly Val Lys Arg  
 210 215 220  
 Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro Ala Val Glu Val  
 225 230 235 240  
 Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu Asp His Gln Thr  
 245 250 255  
 Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg Gln Lys Glu Ala  
 260 265 270  
 Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr Glu Gln Ala Ala  
 275 280 285  
 Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly Leu Leu Glu Glu  
 290 295 300  
 Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly Pro Glu Ala Gly  
 305 310 315 320  
 Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala Thr Thr Glu Lys  
 325 330 335  
 Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val His Arg Leu Arg  
 340 345 350

```

Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg His Gln Glu Leu
      355      360      365
Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu Arg Leu Ala Glu
      370      375      380
Leu Ala Arg Arg Gln Arg Arg Gln Ala Arg Arg Glu Ala Glu Ala
      385      390      395      400
Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln Ala Pro Asp Ile
      405      410      415
Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu Arg Thr Leu Lys
      420      425      430
Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser Phe Gln Arg Arg
      435      440      445
Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys Arg Lys Tyr Lys
      450      455      460
Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile Gln Leu
      465      470      475

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```

<210> 109
<211> 1789
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..94

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<220>
<221> CDS
<222> 95..1252

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<220>
<221> 3'UTR
<222> 1253..1789

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<220>
<221> polyA_signal
<222> 1751..1756

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<220>
<221> polyA_site
<222> 1774..1789

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```

<400> 109
gggtcttgcaa tatttattct gctttcgggt agatgggagg cccggggacc tggctggggt 60
tctgccaagc ttctccgata cccaggtttc ataa atg tgt ttg ttg ctt tcc tgc 115
                               Met Cys Leu Leu Leu Ser Cys
                               -10
cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163
Pro Cys His Pro Ser Ala His Gly Gln Ser Met Trp Ile Glu Arg Thr
      -5      1      5
tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211
Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu
      10      15      20      25
gtg gtg cac atg tcg cag acc aca att agt cct ctg gag aat gcc ata 259
Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile

```

				30					35				40			
gaa	acc	atg	tcc	acg	gcc	aat	gag	aag	atc	ctg	atg	atg	ata	aac	cag	307
Glu	Thr	Met	Ser	Thr	Ala	Asn	Glu	Lys	Ile	Leu	Met	Met	Ile	Asn	Gln	
			45					50					55			
tac	cag	agt	gat	gag	acc	ctc	ccc	atc	aac	cca	ctc	tcc	atg	ctc	ctg	355
Tyr	Gln	Ser	Asp	Glu	Thr	Leu	Pro	Ile	Asn	Pro	Leu	Ser	Met	Leu	Leu	
		60					65					70				
aac	ggg	att	gtg	gac	cct	gct	gtc	atg	gga	ggc	ttc	gcc	aag	tat	gag	403
Asn	Gly	Ile	Val	Asp	Pro	Ala	Val	Met	Gly	Gly	Phe	Ala	Lys	Tyr	Glu	
	75					80					85					
aag	gcc	ttc	ttc	act	gaa	gag	tat	gtc	agg	gac	cac	cct	gag	gac	cag	451
Lys	Ala	Phe	Phe	Thr	Glu	Glu	Tyr	Val	Arg	Asp	His	Pro	Glu	Asp	Gln	
	90				95				100						105	
gac	aag	ctg	acc	cac	ctc	aag	gac	ctg	att	gca	tgg	cag	atc	ccc	ttc	499
Asp	Lys	Leu	Thr	His	Leu	Lys	Asp	Leu	Ile	Ala	Trp	Gln	Ile	Pro	Phe	
			110						115				120			
ttg	gga	gct	ggg	att	aag	atc	cat	gag	aaa	agg	gtg	tca	gat	aac	ttg	547
Leu	Gly	Ala	Gly	Ile	Lys	Ile	His	Glu	Lys	Arg	Val	Ser	Asp	Asn	Leu	
		125						130					135			
cga	ccc	ttc	cat	gac	cgg	atg	gag	gaa	tgt	ttc	aag	aac	ctg	aaa	atg	595
Arg	Pro	Phe	His	Asp	Arg	Met	Glu	Cys	Phe	Lys	Asn	Leu	Lys	Met		
		140					145				150					
aag	gtg	gag	aag	gag	tac	ggt	gtc	cga	gag	atg	cct	gac	ttt	gac	gac	643
Lys	Val	Glu	Lys	Glu	Tyr	Gly	Val	Arg	Glu	Met	Pro	Asp	Phe	Asp	Asp	
	155					160					165					
agg	aga	gtg	ggc	cgt	ccc	agg	tct	atg	ctg	cgc	tca	tac	aga	cag	atg	691
Arg	Arg	Val	Gly	Arg	Pro	Arg	Ser	Met	Leu	Arg	Ser	Tyr	Arg	Gln	Met	
	170				175				180					185		
tcc	atc	atc	tct	ctg	gct	tcc	atg	aat	tct	gac	tgc	agc	acc	ccc	agc	739
Ser	Ile	Ile	Ser	Leu	Ala	Ser	Met	Asn	Ser	Asp	Cys	Ser	Thr	Pro	Ser	
			190					195					200			
aag	cct	acc	tca	gag	agc	ttt	gac	ctg	gaa	tta	gca	tca	ccc	aag	acg	787
Lys	Pro	Thr	Ser	Glu	Ser	Phe	Asp	Leu	Glu	Leu	Ala	Ser	Pro	Lys	Thr	
		205						210				215				
ccg	aga	gtg	gag	cag	gag	gaa	ccg	atc	tcc	ccg	ggg	agc	acc	ctg	cct	835
Pro	Arg	Val	Glu	Gln	Glu	Glu	Pro	Ile	Ser	Pro	Gly	Ser	Thr	Leu	Pro	
		220					225					230				
gag	gtc	aag	ctg	cgg	agg	tcc	aag	aag	agg	aca	aag	aga	agc	agc	gta	883
Glu	Val	Lys	Leu	Arg	Arg	Ser	Lys	Lys	Arg	Thr	Lys	Arg	Ser	Ser	Val	
	235					240					245					
gtt	ttt	gcg	gat	gag	aaa	gca	gct	gca	gag	tcg	gac	ctg	aag	cgg	ctt	931
Val	Phe	Ala	Asp	Glu	Lys	Ala	Ala	Ala	Glu	Ser	Asp	Leu	Lys	Arg	Leu	
	250				255				260					265		
tcc	agg	aag	cat	gag	ttc	atg	agt	gac	acc	aac	ctc	tcg	gag	cat	gcg	979
Ser	Arg	Lys	His	Glu	Phe	Met	Ser	Asp	Thr	Asn	Leu	Ser	Glu	His	Ala	
			270					275					280			
gcc	atc	ccc	ctc	aag	gcg	tct	gtc	ctc	tct	caa	atg	agc	ttt	gcc	agc	1027
Ala	Ile	Pro	Leu	Lys	Ala	Ser	Val	Leu	Ser	Gln	Met	Ser	Phe	Ala	Ser	
			285					290					295			
cag	tcc	atg	cct	acc	atc	cca	gcc	ctg	gcg	ctc	tca	gtg	gca	ggc	atc	1075
Gln	Ser	Met	Pro	Thr	Ile	Pro	Ala	Leu	Ala	Leu	Ser	Val	Ala	Gly	Ile	
		300					305					310				
cct	ggg	ttg	gat	gag	gcc	aac	aca	tct	ccc	cgc	ctc	agc	cag	acc	ttc	1123
Pro	Gly	Leu	Asp	Glu	Ala	Asn	Thr	Ser	Pro	Arg	Leu	Ser	Gln	Thr	Phe	
	315					320					325					

```

ctc caa ctc tca gat ggt gac aag aag aca ctc aca cgg aag aag gtc 1171
Leu Gln Leu Ser Asp Gly Asp Lys Lys Thr Leu Thr Arg Lys Lys Val
330          335          340          345
aat cag ttc ttc aag aca atg ctg gcc agc aaa tcg gct gaa gaa ggc 1219
Asn Gln Phe Phe Lys Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly
          350          355          360
aaa cag atc cca gac tcg ctg tcc acg gac ctg tgagctgctg ctgactaggg 1272
Lys Gln Ile Pro Asp Ser Leu Ser Thr Asp Leu
          365          370
ctgcatggga gagccagggg ggggagtttc tggaagagga aagccatgcg tggaacatcg 1332
aagcctcaga gagtgggaga ctgtcccat cagttgtcct tacttagagg agacagagag 1392
gccaatcagg tccagagct tgaatgctaa caagcccagc atcccctggg gctgtgatca 1452
tggtggatga ggaagcctca acgtagattc ctgaactcaa ggtaccagca agaatgcctt 1512
ctcccagtggt gctctcccca acatcctagg cacagctttc ataaccagt ttcttaggtg 1572
taagaaactg tttttatctc atttattaag tctcagaact taacagaaaa ggaagccttt 1632
taaataattct ttttaatttt attttagatt aacagttttg tactttacat tttttataac 1692
aaccaaccag tttcttttct agccaatcat ctctgaagag ttgctgtttc ttactgacaa 1752
taaaaaatgt tctcttggtt caaaaaaaaa aaaaaaa 1789

```

<210> 110  
 <211> 386  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..15

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<400> 110
Met Cys Leu Leu Leu Ser Cys Pro Cys His Pro Ser Ala His Gly Gln
-15          -10          -5          1
Ser Met Trp Ile Glu Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro
          5          10          15
Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
          20          25          30
Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
          35          40          45
Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
50          55          60          65
Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
          70          75          80
Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
          85          90          95
Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
          100          105          110
Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
          115          120          125
Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
130          135          140          145
Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
          150          155          160
Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
          165          170          175
Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
          180          185          190

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Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
 195                200                205
Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
210                215                220                225
Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
                230                235                240
Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
                245                250                255
Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
                260                265                270
Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
275                280                285
Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
290                295                300                305
Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
                310                315                320
Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
                325                330                335
Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala
340                345                350
Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu Ser Thr
355                360                365
Asp Leu
370

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<210> 111
<211> 1408
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..102

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<220>
<221> CDS
<222> 103..1263

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<220>
<221> 3'UTR
<222> 1264..1408

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<220>
<221> polyA_signal
<222> 1341..1346

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<220>
<221> polyA_site
<222> 1365..1408

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<400> 111
cttcttgact ctctgttcac agaactcagg ctgcctccag ccagcctttg cccgctagac 60
tcactggccc tgatcacttg aaggtgcagc aagtcactga ga atg agc act ttc 114
Met Ser Thr Phe
1

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ttc tgc gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt	162
Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys	
5 10 15 20	
ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc	210
Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser	
25 30 35	
tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg	258
Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu	
40 45 50	
tcc cct ttt tgg ggc ttg atc ctc ttc tgc gtg tca tgc ttc ctc atg	306
Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met	
55 60 65	
tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca	354
Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala	
70 75 80	
gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag	402
Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys	
85 90 95 100	
tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa	450
Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu	
105 110 115	
aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc	498
Asn Gly Pro Gly Ala Glu Glu Leu Arg Thr Cys Ser Pro Arg Leu	
120 125 130	
tgc gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct	546
Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala	
135 140 145	
tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg	594
Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val	
150 155 160	
atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt	642
Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu	
165 170 175 180	
ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act	690
Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr	
185 190 195	
gtg gag gtc aca aag acg ttt ttg cct ctt ctt aga aaa tcc aaa ggg	738
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly	
200 205 210	
agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg	786
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg	
215 220 225	
ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca	834
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser	
230 235 240	
gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc	882
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile	
245 250 255 260	
caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg	930
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp	
265 270 275	
gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag	978
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln	
280 285 290	
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta	1026



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Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg Asn Phe Leu Leu
    295              300              305
ttg atc aac tcg tta gcc agc aag gac ttc tct ccg gtg ctg cgg gac 1074
Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro Val Leu Arg Asp
    310              315              320
atc cag cat gct atc ttg gcg aag agc cct ttt gcc tat tac acg cca 1122
Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala Tyr Tyr Thr Pro
    325              330              335              340
ggg aaa ggc gct tac ttg tgg atc tgc ctt gct cac tat ttg cct att 1170
Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His Tyr Leu Pro Ile
    345              350              355
ggc ata tat gat tac ttt gct aaa aga cat ttt ggc caa gac aag ccc 1218
Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly Gln Asp Lys Pro
    360              365              370
atg ccc aga gct tta aga atg cct aac tac aag aaa aag gcc ccc 1263
Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys Lys Ala Pro
    375              380              385
taggcaatgg aagccctcaa agaagtcgga atgtcatagt cttgaaatga aagggaaact 1323
gggaaattgg gtttctcatt aaagttgttt cccactctgt waaaaaaaaa aaaaaaaaaa 1383
aaaaaaaaaga aaaaaaaaaa aaaaaa 1408

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&lt;210&gt; 112

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

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Met Ser Thr Phe Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro
 1              5              10              15
Thr Val Leu Cys Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly
    20              25              30
Gln Leu Trp Ser Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys
    35              40              45
Leu Leu Ile Leu Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser
    50              55              60
Cys Phe Leu Met Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val
    65              70              75              80
Asp Gln Lys Ala Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His
    85              90              95
Ala Leu Cys Lys Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly
    100              105              110
Val Leu Asn Glu Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys
    115              120              125
Ser Pro Arg Leu Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln
    130              135              140
Ile Lys Asp Ala Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly
    145              150              155              160
Leu Trp Ala Val Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp
    165              170              175
Gly Glu Leu Leu Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn
    180              185              190
Phe Phe Gly Thr Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg
    195              200              205
Lys Ser Lys Gly Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala
    210              215              220

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Pro Val Glu Arg Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr
225                230                235                240
Met Phe Ser Ser Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys
                245                250                255
Val Ala Ser Ile Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr
                260                265                270
Ser Asp Lys Trp Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro
                275                280                285
Ala Glu Val Gln Glu Asp Tyr Cys Gln Asp Tyr Ile Leu Ala Gln Arg
                290                295                300
Asn Phe Leu Leu Leu Ile Asn Ser Leu Ala Ser Lys Asp Phe Ser Pro
305                310                315                320
Val Leu Arg Asp Ile Gln His Ala Ile Leu Ala Lys Ser Pro Phe Ala
                325                330                335
Tyr Tyr Thr Pro Gly Lys Gly Ala Tyr Leu Trp Ile Cys Leu Ala His
                340                345                350
Tyr Leu Pro Ile Gly Ile Tyr Asp Tyr Phe Ala Lys Arg His Phe Gly
                355                360                365
Gln Asp Lys Pro Met Pro Arg Ala Leu Arg Met Pro Asn Tyr Lys Lys
                370                375                380
Lys Ala Pro
385

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